

GenCore version 4.5
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OM nucleic - nucleic search, using sw model
Run on: March 2, 2002, 23:35:23 ; Search time 2023.3 Seconds
(without alignments)
8316.672 Million cell updates/sec
Title: US-08-989-881-1
Perfect score: 1020
Sequence: 1 gttgtaaaacgacgncagt.....gcttgccgtaacatgcat 1020
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 1472140 seqs, 8248589755 residues
Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Result No.	Score	Match	Length	DB	ID	Description
1	822	80.6	822	8	ATU73610	U73610 Arabidopsis
2	652	63.9	1842	8	ATHCDPKA	D21805 Arabidopsis
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4	449	44.0	1998	8	ATU31836	U31836 Arabidopsis
5	449	44.0	2115	8	AF361634	AF361634 Arabidopsis
6	448.4	44.0	2087	6	AX077698	AX077698 Arabidopsis
7	448.4	44.0	2162	6	AX077694	AX077694 Arabidopsis
8	437.2	42.9	1967	6	AX077712	AX077712 Arabidopsis
9	437.2	42.9	1967	6	AF035944	AF035944 Fragaria
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11	432.4	42.4	1896	8	ATU20624	U20624 Arabidopsis
12	421.4	41.3	2313	8	AF276999	AF276999 Funaria h
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24	355.4	34.8	2040	6	OSCDPK2	X81394 O. sativa MR
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26	346.2	33.9	1747	8	ATHCDPKB	D21806 Arabidopsis
27	340.6	33.4	2243	8	TRU82087	U82087 Tortula rur
28	339	33.2	87508	8	AC068602	AC068602 Genomic s
29	337.6	33.1	1998	8	ATU31751	U31751 Arabidopsis
30	336	32.9	1723	6	AX077703	AX077703 Arabidopsis
31	336	32.9	1723	6	ZMD28376	U28376 Zea mays ca
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33	332.8	32.6	2306	6	AX077704	AX077704 Arabidopsis
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35	329	32.3	1975	8	AY034995	AY034995 Arabidopsis
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ALIGNMENTS

RESULT 1

LOCUS	ATU73610	822 bp	mRNA	PLN	02-DEC-1999
DEFINITION	Arabidopsis thaliana ATCDPK1a (cpk1a) mRNA, partial cds.				
ACCESSION	U73610				
VERSION	U73610.1	GI:6502506			
KEYWORDS	thale cress.				
SOURCE	Arabidopsis thaliana				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
REFERENCE	1 (bases 1 to 822)				
AUTHORS	Sheen, J.				
TITLE	Ca2+-dependent protein kinases and stress signal transduction in plants				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 822)				
AUTHORS	Sheen, J.				
TITLE	Direct Submission				

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES


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RESULT 3
LOCUS F25A4 115721 bp DNA PLN 15-SEP-1999
DEFINITION Arabidopsis thaliana chromosome 1 BAC F25A4 sequence, complete
sequence.
ACCESSION AC008263
VERSION AC008263.2 GI:5868932
KEYWORDS HTG.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 115721)
AUTHORS Vysotskai,V.S., Schwartz,J.R., Yu,G., Toriumi,M., Lenz,C., Liu,S.,

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Lee,J.M., Li,J., Gonzalez,A., Liu,A., Liu,K., Vaysberg,M.,
Sakano,H., Chin,C., Choi,E., Chlou,J., Altafi,H., Araujo,R.,
Brooks,S., Ruehler,E., Chao,Q., Conn,L., Conway,A.B., Dunn,P.,
Hansen,N., Howing,B., Huizar,L., Khan,S., Kim,C., Palm,C.,
Rowley,D., Shinn,P., Walker,M., Davis,R.W., Ecker,J.R.,
Federspiel,N.A. and Theologis,A.
Arabidopsis thaliana chromosome 1 BAC F25A4 sequence
Unpublished
2 (bases 1 to 115721)
Theologis,A.
Direct Submission
Submitted (31-JUL-1999) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
3 (bases 1 to 115721)
Theologis,A.
Direct Submission
Submitted (10-SEP-1999) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
4 (bases 1 to 115721)
Theologis,A.
Direct Submission
Submitted (15-SEP-1999) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
On Sep 10, 1999 this sequence version replaced gi:5668776.
The sequence of BAC F25A4 from Arabidopsis thaliana chromosome 1.
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RESULT 4
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DEFINITION Arabidopsis thaliana calmodulin-domain protein kinase CDPK isoform 7 (CPK7) mRNA, complete cds.
ACCESSION U31836
VERSION U31836.1 GI:1399276
KEYWORDS thale cress.
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
JOURNAL 1 (bases 1 to 1998)
AUTHORS Hrabak, E.M., Dickmann, L.J., Satterlee, J.S. and Sussman, M.R.
TITLE The calmodulin-domain protein kinase (CDPK) gene family of
JOURNAL Arabidopsis thaliana contains at least twelve members
REFERENCE Unpublished (1995)
AUTHORS Hrabak, E.M.
TITLE Direct Submission
JOURNAL Submitted (18-JUL-1995) Estelle Hrabak, Horticulture, University of
REFERENCE Wisconsin, 1575 Madison, WI 53706, USA
AUTHORS Location/Qualifiers
TITLE 1. .1998
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source /organism="Arabidopsis thaliana"
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ACCESSION AF361634
VERSION AF361634.1 GI:13605616
KEYWORDS FLI_CDNA.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 2115)
Shinn,P., Chen,H., Cheuk,R., Kim,C.J., Banh,J., Bowser,L.,
Carninci,P., Chung,M.K., Goldsmith,A.D., Hayashizaki,Y., Ishida,J.,
Jones,T., Kaniya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M.,
Lin,J., Liu,S.X., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J.,
Pham,P.K., Quach,H.L., Sakano,H., Sakurai,T., Satou,M., Seki,M.,
Southwick,A., Toriumi,M., Yamada,K., Yu,G., Shinozaki,K.,
Davis,R.W., Theologis,A. and Ecker,J.R.
Arabidopsis cdna clones
Unpublished
2 (bases 1 to 2115)
Shinn,P., Chen,H., Cheuk,R., Kim,C.J., Banh,J., Bowser,L.,
Carninci,P., Chung,M.K., Goldsmith,A.D., Hayashizaki,Y., Ishida,J.,
Jones,T., Kaniya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M.,
Lin,J., Liu,S.X., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J.,
Pham,P.K., Quach,H.L., Sakano,H., Sakurai,T., Satou,M., Seki,M.,
Southwick,A., Toriumi,M., Yamada,K., Yu,G., Shinozaki,K.,
Davis,R.W., Theologis,A. and Ecker,J.R.
Direct Submission
Submitted (15-MAR-2001) Salk Institute Genomic Analysis Laboratory
(SIGAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
USA
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL CDNAs (RAFL CDNA : 'RIKEN
Arabidopsis Full-length CDNA') : Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kaniya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGECC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL CDNAs: Shinn,P., Chen,H.,
Cheuk,R., Kim,C.J., Koesema,E., Meyers,M.C., Tracy,S.E., Banh,J.,
Bowser,L., Chung,M.K., Goldsmith,A.D., Jones,T., Karlin-Neumann,G.,
Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M., Palm,C.J.,
Pham,P.K., Quach,H.L., Sakano,H., Sakurai,T., Southwick,A.,
Tang,C.C., Toriumi,M., Yamada,K., Yu,G., Davis,R.W., Theologis,A.,
and Ecker,J.R.

Shinn,P. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to
this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)
contributed equally to this work as PIs.
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RESULT 6
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DEFINITION Sequence 5 from Patent WO0107592.
ACCESSION AX077698
VERSION AX077698.1 GI:13122073
KEYWORDS Arabidopsis sp.
SOURCE Arabidopsis sp.
ORGANISM Arabidopsis sp.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 2087)
AUTHORS Holt, C.D., White, A.J., Michael, A.J. and Osborn, R.W.
TITLE Herbicide resistant plants and methods for the production thereof
JOURNAL Patent: WO 0107592-A 5 01-FEB-2001;
ZENECA LIMITED (GB)
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QY 893 acccttggatcacgaatgcaaaagaaagagatcaagctt 930
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Db 1138 ACCCATGGATTCAAGACGCAAGAAAGAAAGCTCCCAATGTT 1175
RESULT 7
LOCUS AX077694 2162 bp DNA PAT 22-FEB-2001
DEFINITION Sequence 1 from Patent WO0107592.
ACCESSION AX077694
VERSION AX077694.1 GI:13122069
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 2162)
AUTHORS Holt, C.D., White, A.J., Michael, A.J. and Osborn, R.W.
TITLE Herbicide resistant plants and methods for the production thereof
JOURNAL Patent: WO 0107592-A 1 01-FEB-2001;
ZENECA LIMITED (GB)
FEATURES
source Location/Qualifiers
1. 2162
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 601 a 409 c 522 g 630 t
-ORIGIN

Query Match 44.0%; Score 448.4; DB 6; Length 2162;
Best Local Similarity 71.8%; Pred. No. 2e-122;
Matches 587; Conservative 0; Mismatches 231; Indels 0; Gaps 0;

QY 113 agatcagcgacaagtacatcttagcagcaactcggctgcgcgcaattcggatcaact 172
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Db 358 ACATCGAGAGCGGTACTACTACGACAGAGACTCGCGCGGAGTTGGTGTCACCT 417
QY 173 atcttgtacagatagagagactcgtgaagctttagcttgcgaatcaatctccaagagaa 232
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Db 418 ACCTCTGTATCGAGAGTCCCTCGCGTGACCTACTCGCTGCAATCGATCTCCAGAGGA 477
QY 233 agctccgaacgcgcgtcgaatgtgaagcgtccgctgcggaactcagatcagatcaact 292
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Db 478 AGCTTAGAAGTCTGTGGATATGAAGATGTTAAAGAGAGAGTAGCGATTATGAAGCATT 537
QY 293 tacoggaacaccccaacgctgtgaacttaagcgactatgagataacgagacgcgtgc 352
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Db 538 TGCCCTAAGAGTTCGAGTATGTTACTTTGAAGAGAGCTGTGAGGATGATATGCTGTGC 597
QY 353 atcttgtatagagcttctgaagagtgagctgttcttggctggatgttgcgaagagac 412
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Db 598 ATTGGTTATGAGCTTGTGAAGTGGCGAGCTTTTCATCGGATTTGTCGAGAGTGC 657
QY 413 attatcacagagcgtgcgcgcgtacgtcgcgagaaacatcgcggaagtgtgagatgt 472
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Db 658 ATTATACGAGCGTCTGCTGCTGCTGTACTTAAGACATATGTTGAGGTGTGCGAGCTTT 717


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QY 473 gtcattgcaatggtgttatgcatagagatttgaagcctgagaaatttttttgcataaa 532
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QY 533 agaagagaaattctgcaacttaagcctatgatttggttttatctgttcttttaaacctg 592
Db 778 AGAAGAGAACCTGCGCTTTGAAGCTATTGATTTTGGATTGTCGATTTCCTCAAGCCAG 837
QY 593 gagagaggtttacagagatttgggaagctcttattatatggtcgcagagtggttgaaga 652
Db 838 GTGAGAAATCTCTGAGATTGTTGGGAGCTCATATTACATGGACCTGAGGCTGTTAAGC 897
QY 653 gaaattatggaccagaggttgatgtgtgagtgctggagttatcctctacatcttcttt 712
Db 898 GGAATTATGAGACCGAATAATAGATATTGAGTGTCTGAGTGATTCATTATCTCTGT 957
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Db 1078 TCAGACAAATGTAGACCTGATCCAAAGCGCTGACTGCAAAAGCAAGTCTTGAGC 1137
QY 893 acccttggtacagagatgcaagaaaggatcaagctt 930
Db 1138 ACCCATGGATTTCAGAACGCAAGAAAGCTCCCAATGTT 1175

RESULT 8
LOCUS AX077712 1967 bp DNA PAT 22-FEB-2001
DEFINITION Sequence 19 from Patent WO0107592.
ACCESSION AX077712
VERSION AX077712.1 GI:13122087
KEYWORDS
SOURCE Fragaria x ananassa.
ORGANISM
Fragaria x ananassa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Rosales; Rosaceae; Fragaria.
1 (bases 1 to 1967)
Holt, C.D., White, A.J., Michael, A.J. and Osborn, R.W.
Herbicide resistant plants and methods for the production thereof
Patent: WO 0107592-A 19 01-FEB-2001;
ZENCA LIMITED (GB)
FEATURES
Location/Qualifiers
source 1..1967
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BASE COUNT 572 a 334 c 500 g 561 t
ORIGIN

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Best Local Similarity 71.2%; Pred. No. 4.2e-119;
Matches 577; Conservative 0; Mismatches 233; Indels 0; Gaps 0;

QY 109 actcagatcagcagcaagatcatctttagacagaaactcgtcgcgcgaattcggaaac 168
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QY 169 acgtatctttgacagatagagaaactcgtgaagcttttagttgcaaatcaatctccaag 228
Db 223 ACGTATCTGTCTACTGACAGCCGCCAACGAGAACTACGCTTGCAATCATCATCGAAG 282
QY 229 agaagctccgaacccgcgtcgatgtggaagacgtccgcgtgtagtcacacatcatgca 288
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QY 289 actttaaccggaacacacccaaacgttgtaaaacttaaacgacttatgaggataacgagacc 348
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Db 403 GTCCATCTTGTGTTAGGAGCTCTGTGAGGGCGGTGAGCTTTTGTATCGGATCGTGCTAGG 462
QY 409 ggacattatcacagagcgtgcgcggtctaccgtcgcgagaaacgacatcgcggaagttgag 468
Db 463 GGACANTACACTGAGCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 522
QY 469 atgtcgtcgtcgaatggtgttatgcatagagatttgaagcctgagaaattcttctgttgc 528
Db 523 ATGTGCCCAAGCATGCTGTGATGTCACCGGATCTTAAACCTGAGAACCTTTTGTGTTGCA 582
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Db 943 GATCATACTTGTGCTGCAAAATGCAAGAGA 972

RESULT 9
LOCUS AF035944 1967 bp mRNA PLN 09-DEC-1997
DEFINITION Fragaria x ananassa calcium-dependent protein kinase (MAX17) mRNA, complete cds.
ACCESSION AF035944
VERSION AF035944.1 GI:2665889
KEYWORDS
SOURCE Fragaria x ananassa.
ORGANISM
Fragaria x ananassa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Rosales; Rosaceae; Fragaria.
1 (bases 1 to 1967)
Llop-Tous, J., Dominguez-Puigjaner, E. and Vendrell, M.
Submitted (26-NOV-1997) Agrobiologia, CSIC, Jordi Girona 18-26,
Barcelona 08034, Spain
Location/Qualifiers
source 1..1967
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CDS 28..1617
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QY 724 ccgttttggcacagactgaacaggtgtgctcttgccttgccttggagggagttcttgat 783
Db 660 CCAITTTGGCCGAGACTGACAGAGGGTGTGCTCAGCGCATCATTAGTCACTATCGAC 719
QY 784 tttaagagagatcttggctgcagatatacagagagcgaagagccttgggaagcagatg 843
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QY 844 ttggaacctgattcaactaagcgtttgactgtcagcaagttcttgcacaccttgata 903
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RESULT 11
ATU20624
LOCUS
DEFINITION
Arabidopsis thaliana calcium-dependent protein kinase (CDPK19)
mRNA, complete cds.
ACCESSION
U20624
VERSION
U20624.1 GI:836941
KEYWORDS
SOURCE
thale cress.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 1896)
AUTHORS
Hong, Y., Takano, M., Liu, C.M., Gasch, A., Chye, M.L., Tan, C.T.,
Koh, C.C. and Chua, N.H.
TITLE
Expression of the Calcium-Dependent Protein Kinase Gene Family in
Arabidopsis thaliana
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 1896)
AUTHORS
Hong, Y.
DIRECT SUBMISSION
Submitted (03-FEB-1995) Yan Hong, National University of Singapore,
Institute of Molecular and Cell Biology, 10 Kent Ridge Crescent,
Singapore, 0511, Republic of Singapore
FEATURES
Location/Qualifiers
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QY 184 gatagagagactcgtaaagcgttttagcttgcataatcaatcccaagagaagagcgtccgaac 243
Db 290 GATATCAAAACGGCGGAGAGATGCGTCAAGTCTATATCAAAAGAAAGAGCTTAGAACA 349
QY 244 gccgtgatgtggaagacgtccctcgtggaatcacatcatcgtcaactttaccggaacac 303
Db 350 GCTGTGATATAGAGGATGTTAGGAGGAAGTTGAGATATGAACATATGCCATAGACAC 409
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QY 364 gacgtttgaaagaggtgagcgttttggcgaattgttgcgaagacattatcacagag 423
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RESULT 12
LOCUS
DEFINITION
Funaria hygrometrica calcium-dependent protein kinase gene, partial
cgs.
ACCESSION
AF276999
VERSION
AF276999.1 GI:14484894
KEYWORDS
SOURCE
Funaria hygrometrica.
ORGANISM
Funaria hygrometrica

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Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Bryopsida;
Funariaceae; Funariales; Funariaceae; Funaria.

REFERENCE
AUTHORS Mitra,D. and Johri,M.M.
TITLE Genomic DNA clone of a calcium-dependent protein kinase from the moss Funaria hygrometrica

JOURNAL ncss Funaria hygrometrica
UNPUBLISHED
DOI
PMID
 accession number 2 (bases 1 to 2313)
Mitra,D. and Johri,M.M.
Direct Submission
Submitted (12-JUN-2000) Department of Biological Sciences, Tata Institute of Fundamental Research, Homi Bhabha Road, Mumbai, Maharashtra 400 005, India

JOURNAL Location/Qualifiers
FEATURES
source location 1..2313
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mRNA <1..>1557
CDS <1..>1557
product="calcium-dependent protein kinase"
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BASE COUNT 558 a 449 c 717 g 589 t
ORIGIN

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Best Local Similarity 70.5%; pred. No. 2.e-114;
Matches 563; Conservative 0; Mismatches 236; Indels 0; Gaps 0;

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QY 541 aattctgcacttaaaggctattgatttgggttattctgtctctttaacctggagagg 600
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Db 532 AATTGCGCGGTGAAGCCATCGACTTCGCGGTGTCTGTGTCTTTCACAGCCAGGGGAAAAG 591

JOURNAL

Submitted (22-JAN-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA

COMMENT

On Dec 15, 1999 this sequence version replaced gi:6041764.

e-mail for correspondence: arab@sequence.stanford.edu
Genes with similarity to proteins in the databases are described
as 'putative', '-like', or 'similar to'. Genes that have EST
similarity but no significant protein similarity are described as
'unknown proteins'. Genes that are annotated based only on gene
prediction software are described as 'hypothetical proteins'. The
software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
<http://complib.ornl.gov/section/index.html>), GENSCAN (Chris Burge,
<http://genomic.stanford.edu/~chris/GENSCANW.html>), Fexa (V. Solovyev
& A. Salamov, Sanger Centre, <http://genomic.sanger.ac.uk/>), and
NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, <http://www.cbs.dtu.dk/NetPlantGene.html>).

FEATURES
source

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/db_xref="taxon:3702"

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5621..5788,5881..6111,6229..6402)

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PGADQFPKKEKRGIESEFFNNYFTTFAQVSLIIVYQSNVSVSGLIAPAI
LMLLCIIFPAGSLYVKVKGASGPIHSTRTVVAIKRRKLPQGVNLYNVIASDF
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gene

CDS

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complement(join(18661..19422,19510..19623,19837..20376))

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/note="Hypothetical protein"

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23743..24942

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gene

CDS

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40123..40177.40266..40561))
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/codon_start=1
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/translation="MDCIKTGRSAFVAIAPEFPFAAGTMAGAVDLFSSSANLIF
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Query Match          37.7%; Score 384.4; DB 8; Length 108767;
Best Local Similarity 67.7%; Pred. No. 5.9e-103;
Matches 693; Conservative 0; Mismatches 106; Indels 225; Gaps 2;

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QY	215	aatcaatctccaagagaaagctccgaaccgcctcgatgtggaagacgtccgctcgtgaag	274
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QY	575	ctgtctctctttaaaccct	591
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DEFINITION	Sequence 20 from Patent WO0107592.	PAT	22-FEB-2001
ACCESSION	AX077713		
VERSION	AX077713.1	GI:13122088	
KEYWORDS			
SOURCE	liverwort.		
ORGANISM	Marchantia polymorpha		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta;		
	Marchantiophyta; Marchantiales; Marchantiaceae; Marchantia.		
	1 (bases 1 to 1647)		
	Holt, C.D., White, A.J., Michael, A.J. and Osborn, R.W.		
	Herbicide resistant plants and methods for the production thereof		
	Patent: WO 0107592-A 20 01-FEB-2001;		
	ZENECA LIMITED (GB)		
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237	CAATTACACCTCGAGCGGAACCTGGTCGNGGCAGTTGGTGTCTACGCAGTTTGTGTAC	296			
QY 183	agatagagacactcgtaagaacttttagcttgcacatacaatctccaaagagaagctccgaac	242			
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297	GCACAAGTTACAGGTGAGCTTTTAGCTCGCAATGCTCAATTCGAAGAGGAAGTTGACCAA	356			
QY 243	cgcgtcgatgtgaagacgtccgctcgtaagtcacgcatcatgtcaactttacgggaaca	302			
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357	TAAGGATGACGTAGAGGATGTTTCGGAGGGAAGTGCAGATCATCGACCACTTTAGAGGGGCA	416			
QY 303	cccaaacgctgtgaacttaaacgcgacttatgaggataacgagacgctgcactcttgtgat	362			
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417	GAAACAATGTGCAATTGAAGGGGCCATGAGGATAAACACACAGTGCATCTCGTCAT	476			
QY 363	ggagctttgtgaaggaggtgagcttttttggtcgattgttgcgaagggaattacaga	422			
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477	GGAGCTTTGCTGGCGGAGACTCTTCACCCGCAATTATTCACGGGGGCCACTACAGTGA	536			
QY 423	gcgtgcggcggtacgctgcgagacgacatcgcggaagttgtgaggtatgtcatgtcaa	482			
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537	GAGGCGTGTGCAGCTCTATGTAGAACATATAGTGAAGTGTTCACACGTGCCATTTCTCT	596			
QY 483	tggtgttatgcatagatttgaagcctgagaattcttctgtttgtctaaacaagagagaa	542			
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597	GGCAGTTATGACCCGGGATCTGAAGCCGAGAAATTTCTGCTTGTCTAACAGAAGGAGA	656			
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LOCUS AX077714 1647 bp DNA PAT 22-FEB-2001
DEFINITION Sequence 21 from Patent WO0107592.
ACCESSION AX077714
VERSION AX077714.1 GI:13122089
KEYWORDS liverwort.
SOURCE Marchantia polymorpha
ORGANISM Marchantia polymorpha
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Marchantiophyta; Marchantiales; Marchantiaceae; Marchantia.
1 (bases 1 to 1647)
AUTHORS Holt,C.D., White,A.J., Michael,A.J. and Osborn,R.W.
TITLE Herbicide resistant plants and methods for the production thereof
JOURNAL Patent: WO 0107592-A 21 01-FEB-2001;
ZENECALIMITED (GB)
FEATURES
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/organism="Marchantia polymorpha"
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BASE COUNT 445 a 348 c 464 g 390 t
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Query Match 36.0%; Score 367.2; DB 6; Length 1647;
Best Local Similarity 66.9%; Pred. No. 2.9e-98;
Matches 522; Conservative 0; Mismatches 258; Indels 0; Gaps 0;

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Db 536 GAGGCTCTGTCAGCTCTATGTAGAACTATAGTGAAGTGGTTACAGACGTGCCATCTCT 596

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Search completed: March 3, 2002, 00:38:05
Job time: 3762 sec

Result No.	Score	Query %		Length	DB	ID	Description
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1	1016	99.6		1020	19	AAV36878	Nucleotide sequence
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3	448.4	44.0		2162	22	AAAF74262	Arabidopsis calciu
4	443.2	43.5		1836	21	AAAF74633	Arabidopsis thalia
5	437.2	42.9		1967	22	AAAF74280	strawberry calciu
6	432.4	42.4		1726	22	AAAF74263	Arabidopsis calciu
7	367.2	36.0		1647	22	AAAF74281	Liverwort calciu
8	367.2	36.0		1647	22	AAAF74282	Liverwort calciu
9	358.4	35.1		2363	22	AAAF74284	Common ice plant c
10	354.4	34.8		2040	22	AAAF74278	Rice calciu depen
11	354	34.7		1392	21	AAAC48741	Arabidopsis thalia

DR P-PSDB; AAW49837.

PT Protecting plants against environmental stress - by introducing
PT protein kinase domain-containing gene, calcium dependent protein
PT kinase gene or calcium/calmodulin-dependent gene
XX

PS Claim 17; Fig 5; 62pp; English.

This is the nucleotide sequence of the ATCDPK1a protein kinase (PK) domain isolated from the *Arabidopsis* cDNA library, and used in the method of the invention to protect plants against environmental stresses. The methods can be used for improving the tolerance of plants to environmental stresses such as drought, salinity, cold and heat. They provide for increased production efficiency, as well as for improvements in quality and the yield of crop plants and ornamentals. The methods contribute to the production of high quality and high yield agricultural products, e.g. fruits, ornamentals, vegetables, cereals, and field crops.

Sequence 1020 BP; 265 A; 194 C; 280 G; 277 T; 4 other;

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Query Match          99.68;  Score 1016;  DB 19;  Length 1020;
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Matches 1020;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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	QY		
121	QY	gacaagtacatcttaggacgagaaactcgtgcgcgggaattcggaaatcgcgtattt	180
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241	QY	acgcgcgtgatgtggaagacatccgctcgtaatcacgatactgcaacttaccgcgaa	300
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541	b	aattctgcacttaaggctatgatttggtttatctgttctcttaaacacctggagaagg	600
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661	QY	ggaccagaggttgatgtgtggagtcgtggagttaccttcacatctgtctttgttggtt	720
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Qy	721	cctcgcgttttgccgagagactgaacaaagtggtggtcttggccatcttgaggaggattctt	780
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Qy	781	gattttaagagagatcccttgctcgagatatcagagagcgcaaaagacctgtgaagcag	840
Dc	781	gattttaagagagatcccttgctcgagatatcagagagcgcaaaagacctgtgaagcag	840
Qy	841	atggttgaaacctgattcaactaaagcgttttgactgctcagcaagttcttgacacacctgg	900
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Qy	961	ggtaaccagcttngttcccttaagtgaaggttaatttcgagcttggcgttaatcatgtcat	1020
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RESULT 2
AAAF74266
ID AAAF74266 standard; DNA; 2087 BP.

AC AAF74256;
XX
DT 04-MAY-2001 (first entry)

DE Arabidopsis calcium dependent protein kinase clone #1.
XX
KW Calcium dependent protein kinase; CDPK; herbicide resistance;
XW paraquat; diquat; crop production; ds.
xx

OS *Arabidopsis* sp.

PN WO200107592-A2.

PD 01-FEB-2001.

26-JUL-2000; 2000WO-GB02876

AA
PR 27-JUL-1999: 99GB-0017642

AA
PA (ZENE) ZENECA LTD

PI Holt CD, White AJ, Michael AT October 1977

WPI: 2001-168549/77

PT Producing herbicide resistance plants by inhibiting calcium dependent
 PT protein kinase in plants or by providing an intracellular vacuolar
 PT transporter capable of transporting agrochemical into plant vacuole
 XX
 PS Claim 17; Page 33; 50pp; English.

The present invention describes a method of producing plants which are resistant to the herbicides paraquat and diquat, involving inhibiting in the plants a calcium dependent protein kinase (CDPK) and selecting those plants which are resistant to the agrochemical of interest. This is useful in the production of crops with herbicide resistance.

SQ Sequence 2087 BP; 580 A; 391 C; 505 G; 611 T; 0 other;

Query Match 44.0%; Score 448.4; DB 22; Length 2087;
Best Local Similarity 71.9%; Pred. No. 8.5e-127;
Matches 587; Conservative 0; Mismatches 221; Indels 0; Gaps 0;

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Db 358 acatcagaggaccgttaacttactcagacagaaactcgcgccggcgagatttggtttcacctt 417

QY	173	atctttgtacagatagagagactcgtgaagctcttttagcttgcacaaatcattccaaagaa	232
Db	418	acctctgtatcgagaggtcctcgctgacctactcgcttgcacatcgatctccaaagga	477
QY	233	agctcgaaacccgcgtcgatgtggaagacytccgtcgtgaagtcacacgatcatgtcaact	292
Db	478	agcttgaaactcgttgggatatgaagatgttaaaagagaagtagcgattatgaagcatl	537
QY	293	tacggaaacaccacaaacgttctgaaacttaagacgaacttatgagataacgagaccgtgc	352
Db	538	tgacctaaagattcgagattgttacttctgaaagaagcttctggagtgatgaatcgtctgc	597
QY	353	atcttctgatgagctttgtgaagaggtgagctttttgtcgagattgtgcaagaggaac	412
Db	598	atttggtatgagctttgtgaagtgcgagcttttcgacgagattcgtcgagagaggttc	657
QY	413	attatcacagagctgcgcgcctaccgtcgcgagacgatacgcggaagtttggagatgc	472
Db	658	attatcagagcgtcgtcgtcgtcgtgtgttactaagactattgtgagttgtgcagcttt	717
QY	473	gtcatgtcaatggtttatgcatagagatttgaagcctgaagaattctctgttgcataaca	532
Db	718	gtcataagcatgggtgatctcatagagatttgaagccgagaactttttgttgcataa	777
QY	533	agaaaggaaattcgcacttaagcgtattgatttggtttattcgttctcttlaaacctg	592
Db	778	agaaaggaaactcgccttggaaactattgatitggattgtcgatttcttccagccag	837
QY	593	gagagaggtttacagagattgttggaaagtccattattatgtgcctcagaagtgttgaaga	652
Db	838	gtgagaattctcttgattgttgggagtcacattattacatggcaactgaggtgcttaagc	897
QY	653	gaattatggaccagaggttgaagtgttggagtgctgagttactcctacattcttgcctt	712
Db	898	ggaattatggaccgaaatagatatatttgagtgctggagtgattcttatctctctctgt	957
QY	713	gtggtgttctccgttttggcgagagactgaacaaggttggtcctcttgcactcttgaggg	772
Db	958	gttgagtttctccgttcttgccgagagtcagacaagggaggtgtcctcagctattctgcgtg	1017
QY	773	gagttctgtatttaagagagatccttggtcgcagatatcagagagcgcaagagccttg	832
Db	1018	gagtaattgtatttaagaggggaacccgtggcgaacacattctgagacgcgctaagaatcag	1077
QY	833	tgaagcagatgttggaaacctgattcaactaaagcttttgactcgtcagcaagattcttgcac	892
Db	1078	tcagacaaattgttagagctgatcccaagcgtcggtctgactgcgaagcaggtgctgagc	1137
QY	893	accttggatcacagaatgcaagaagaaagatcaagctt	930
Db	1138	acctatggattcgaacgcaagaagctcccaatggt	1175

RESULT	3	
AAAF74262		
ID	AAAF74262	standard; DNA; 2162 BP.
XX	AC	
XX	AAAF74262;	
XX		
DT	04-MAY-2001	(first entry)
XX		
XX		
DE	Arabidopsis	calcium dependent protein kinase clone 23-1.
XX		
KW	Calcium dependent protein kinase;	CDPK; herbicide resistance;
KW	paraquat; diquat;	crop production; ds.
XX		

OS Arabidopsis sp.
 XX
 PN WO200107592-A2.
 XX-
 PD 01-FEB-2001.
 XX
 PF 26-JUL-2000; 2000WO-GB02876.

27-JUL-1999; 99GB-0017642.
(ZENE) ZENECA LTD.
Holt CD, White AJ, Michael AJ, Osborn RW;
WPI; 2001-168549/17.
Producing herbicide resistance plants by inhibiting calcium dependent
protein kinase in plants or by providing an intracellular vacuolar
transporter capable of transporting agrochemical into plant vacuole -
Claim 17; Page 31; 50pp; English.
The present invention describes a method of producing plants which are
resistant to the herbicides paraquat and diquat, involving inhibiting in
the plants a calcium dependent protein kinase (CDPK) and selecting those
plants which are resistant to the agrochemical of interest. This is
useful in the production of crops with herbicide resistance.
Sequence 2162 BP; 601 A; 409 C; 532 G; 570 T; 601 A

Query Match	44.0%;	Score 448.4;	DB 22;	Length 2162;
Best Local Similarity	71.8%;	Pred. No. 8,6e-127;		
Matches 587;	Conservative	0;	Mismatches 231;	Indels 0;
QY	113	agaatcagcgaacagttacatctcttagcagcaactcggctcgccgcgaattccgaatccagt	172	
Db	358	acatcgaggaccgttacttacttcgcacagaaactcggcgcgcggttggtgcactt	417	
QY	173	atctttgtcacatagagagactcgtgaagctttagcttgaatacaatctcccaagagaa	232	
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Db	478	agctttagaactcgtgtgatattgaagatgttaaaagaagtagcgttatgaagcatt	537	
QY	293	taccgggaacacccaaacgttgtgaaccttaagaacttatgagacacttatgagataaocgagaccgtgc	352	
Db	538	tgcttaagagttcagatgttttactttgaagaagcgttgtgaggaataagctgtgc	597	
QY	353	atctttgtgatggagcttttgtgaaggggtgagctttttgtcgcgatgtgtgcgaagagac	412	
Db	598	atttggttatggagcttttgtgaaggtggcagcttttcgatcggatgtgttgcgagaggtc	657	
QY	413	attatcacagacgtgcgcggcctccgtcgcgagaacgatcgcggaagtttgtgagatgt	472	
Db	658	attatcggagcgtgcgtgcgtgtgttactaagactattgttgaggttgtcagcttt	717	
QY	473	gtcatgtcaatgggtgttatgcatagagatttgagcctgagaatttcttgttgcataca	532	
Db	718	gtcataagcatgggtgatcatagagatttgaagccgagaacttttgttgcataa	777	
QY	533	agaagggaattctgcacttaaggctattgatttgggtttatctgtctcttttaaacctg	592	
Db	778	agaagggaactgcctttgaaagctattgatttggattgtcgatttcttcaagccag	837	
QY	593	gaagagagtttacagagatttgtgaagctccttatatatgctccagagtggttgaaga	652	
Db	838	gtgagaaattctctgagatttgtggagttccattacatggcacctgaggtcgttaagc	897	
QY	653	gaatattgacacagaggttgatgtgtgagtgctgagttatctctacatttgcctt	712	
Db	898	ggaattatgacccgaataagatatttggagtgctggagtgacttttatctctctgt	957	
QY	713	gtgggttctctcgttttggcagacactgaacaaggttggtccttgcatttgagg	772	
Db	958	gtggagttctctcgttctgtggcagagtcagacagggagttgctcaggctattctgcgtg	1017	
QY	773	gagttcttattttaagagagatccttggctgcagatatcagagagcgaagagcctgtg	832	

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Db 1018 gagtaattgattttaagaggggaacccgtggccaaacattctgagaccgctaagaatctag 1077
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Db 1078 tcagacaaatgttagcctgattccaaagcgtcggctgactgcaagcaagtgcttgagc 1137
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Db 1138 acccatgattcagaacgcaagaagatcccaatggt 1175

RESULT 4
AAC47633
ID AAC47633 standard; DNA; 1836 BP.
AC AAC47633;
XX
DT 18-OCT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 54543.
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN BP1033405-A2.
PD
PF 06-SEP-2000.
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
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PR 25-MAY-1999; 99US-0135629.
PR 27-MAY-1999; 99US-0136021.
PR 28-MAY-1999; 99US-0136392.
PR 01-JUN-1999; 99US-0136782.
PR 03-JUN-1999; 99US-0137222.
PR 04-JUN-1999; 99US-0137528.
PR 07-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 14-JUN-1999; 99US-0138847.
PR 16-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 17-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
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PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
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PR 24-JUN-1999; 99US-0140354.
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PR 28-JUN-1999; 99US-0140823.
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PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142154.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
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PR 14-JUL-1999; 99US-0143624.
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PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145087.
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PR 23-JUL-1999; 99US-0145218.
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PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 28-JUL-1999; 99US-0145919.
PR 02-AUG-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 04-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 05-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 06-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
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PR	10-AUG-1999;	990S-0148171.	Db	390	tgagatcgagctctaaatcacogttgggagagagctaggtcgtagaattcgggtgttac	449
PR	11-AUG-1999;	990S-0148319.				
PR	12-AUG-1999;	990S-0148341.	QY	171	gtatcttgtacagatagagactcgtgaagcttttagcttgcaaatcaactccaagag	230
PR	13-AUG-1999;	990S-0148565.				
PR	13-AUG-1999;	990S-0148684.	Db	450	gtatctatgtactgataagagacagcgcttttctgttaaatcgatttgaagaa	509
PR	16-AUG-1999;	990S-0149368.				
PR	17-AUG-1999;	990S-0149175.	QY	231	aaagctccgaaccgcgctcgatgtggaagacgctcgctcgctgaagtcacatcatcgaac	290
PR	18-AUG-1999;	990S-0149426.				
PR	20-AUG-1999;	990S-0149722.	Db	510	gaagctgagacagctgtgtgatattgaagatgttagagagaggttgagatttagagca	569
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PR	23-AUG-1999;	990S-0149929.	QY	291	ttaccgggaacaccccaaacgctgtgaaacttaagcgacttatagataacagagacgct	350
PR	23-AUG-1999;	990S-0149930.				
PR	25-AUG-1999;	990S-0150566.	Db	570	tatgctgagacatccctaattgtgttactttgaaggagacttatgaggtgagcatgctg	629
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PR	27-AUG-1999;	990S-0151065.	QY	351	gcatttgtgatggagctttgtgaaggaggtgagctttttggctggtttgctgaagag	410
PR	27-AUG-1999;	990S-0151066.				
PR	27-AUG-1999;	990S-0151080.	Db	630	tcatttgggttatggagctttgtgaaggtgtgaattgtttgatagattgtgtgtagag	689
PR	30-AUG-1999;	990S-0151303.				
PR	31-AUG-1999;	990S-0151438.	QY	411	acattatcacagagcgtgcgcggctaccgtcgcgagaaacgacgcgcggaagttgtgag	470
PR	01-SEP-1999;	990S-0151930.				
PR	07-SEP-1999;	990S-0152363.	Db	690	gcattatactgagagagctgctgctgtctgcactaagacacatcatggaagttgttcag	749
PR	10-SEP-1999;	990S-0153070.				
PR	13-SEP-1999;	990S-0153758.	QY	471	gtgctcatgtcaatggtgttatgcataagattttgaagcctgagaatttcttctgtgctaa	530
PR	15-SEP-1999;	990S-0154018.				
PR	16-SEP-1999;	990S-0154039.	Db	750	gtgtcataagcatggggttaatgcacagggacactgaaacctgagaacttcttctgtgaa	809
PR	20-SEP-1999;	990S-0154779.				
PR	22-SEP-1999;	990S-0155139.	QY	531	caagaaggagaaattctgcacttaaggctattgatttggatttcttcttcttcttctaa	590
PR	23-SEP-1999;	990S-0155486.				
PR	24-SEP-1999;	990S-0155659.	Db	810	caagaaggagactgcacctcttaaggcgattgatttggctctctctctctctctctct	869
PR	28-SEP-1999;	990S-0156458.				
PR	29-SEP-1999;	990S-0156596.	QY	591	tggagagaggtttacagagattgttggagcttcttattatattggtccagaggtttgaa	650
PR	04-OCT-1999;	990S-0157117.				
PR	05-OCT-1999;	990S-0157753.	Db	870	agggagaggttttaacgaaatcgttggtagtccgtactacatgggtcccgaggtgtctaa	929
PR	06-OCT-1999;	990S-0157865.				
PR	07-OCT-1999;	990S-0158029.	QY	651	gagaaattatgaccagaggttgatgtgtggagtgctgaggttatctctacatcttctg	710
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PR	12-OCT-1999;	990S-0158369.	Db	930	acggaaattatggtccagaggttatgttggagtgaggtgaaattcttctacatactgct	989
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PR	14-OCT-1999;	990S-0159637.				
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PR	21-OCT-1999;	990S-0160770.	Db	1110	tatcaggaaaaatgcttgcctgaccacaaagcgtctgtcttacagctcaacaaagctaga	1169
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PR	22-OCT-1999;	990S-0160981.	Db	1170	tcacctgtgttacagaatgcaaaagaa	1197
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PR	23-OCT-1999;	990S-0161404.				
PR	25-OCT-1999;	990S-0161405.				
PR	25-OCT-1999;	990S-0161406.				
PR	26-OCT-1999;	990S-0161359.				
PR	26-OCT-1999;	990S-0161360.				
PR	26-OCT-1999;	990S-0161361.				
PR	28-OCT-1999;	990S-0161920.				
PR	28-OCT-1999;	990S-0161922.				
PR	28-OCT-1999;	990S-0161932.				
PR	29-OCT-1999;	990S-0161933.				
PR	29-OCT-1999;	990S-0162142.				

RESULT 5

AAF74280

ID AAF74280 standard; DNA; 1967 BP.

XX AAF74280;

AC AAF74280;

XX

XX

DT 04-MAY-2001 (first entry)

XX

DE Strawberry calcium dependent protein kinase clone.

XX

KW Calcium dependent protein kinase; CDPK; herbicide resistance;

XX paraquat; diquat; crop production; ds.

OS Fragaria x ananassa.

XX

PN WC200107592-A2.

Query Match 43.5%; Score 443.2; DB 21; Length 1836;
 Best Local Similarity 71.8%; Pred. No. 3.1e-125;
 Matches 580; Conservative 0; Mismatches 228; Indels 0; Gaps 0;


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Db 180 gctgtgatatagagggttagagggaagttagagataatgaacatatgcctagacac 239
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Db 240 ccaaatatcgtgcgtgaaggatgccttgagagatgatgacagtgcatatagtattg 299
QY 364 gaggcttggaaagagtgagcttttggctgcgagattgttgcgaagagacacattatacagag 423
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QY 444 cgtgcggcgctaccgtgcgcgaacagatcgcggaaagtgtgagagtggttcactgtcaat 483
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QY 904 cagaatgcaagaa 917
Db 840 caaaatgcgaagaa 853

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RESULT 7

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ID AAF74281
XX AAF74281 standard; DNA; 1647 BP.
AC AAF74281;
XX
XX
XX
XX
XX 04-MAY-2001 (first entry)
XX Liverwort calcium dependent protein kinase clone #1.
XX
XX Calcium dependent protein kinase; cdpk; herbicide resistance;
XX paraquat; diquat; crop production; ds.
XX
XX Marchantia polymorpha.
XX
XX WO200107592-A2.
XX
XX 01-FEB-2001.
XX
XX 26-JUL-2000; 2000WO-GB02876.
XX
XX 27-JUL-1999; 99GB-0017642.
XX
XX (ZENE ) ZENECA LTD.
XX

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PI Holt CD, White AJ, Michael AJ, Osborn RW;
XX WPI; 2001-168549/17.
DR
XX
XX Producing herbicide resistance plants by inhibiting calcium dependent
PT protein kinase in plants or by providing an intracellular vacuolar
PT transporter capable of transporting agrochemical into plant vacuole -
XX Claim 18; Page 42; 50pp; English.
PS
XX
XX The present invention describes a method of producing plants which are
CC resistant to the herbicides paraquat and diquat, involving inhibiting in
CC the plants a calcium dependent protein kinase (CDPK) and selecting those
CC plants which are resistant to the agrochemical of interest. This is
CC useful in the production of crops with herbicide resistance.
XX
SQ Sequence 1647 BP; 447 A; 349 C; 465 G; 386 T; 0 other;

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Query Match 36.0%; Score 367.2; DB 22; Length 1647;
Best Local Similarity 66.9%; Pred. No. 5.1e-102;
Matches 522; Conservative 0; Mismatches 258; Indels 0; Gaps 0;
QY 123 caagtacatcttggacgagaactcgtgcgcgaattcgggaatcgcgttatctttgtac 182
Db 237 cattcacacctcggacgggaactggtgtgctcagtttgggtgcacgattgtgtac 296
QY 183 agatagagagactcgtgaagcttttagcttgcgaatcaatcgaagagaagctccgaac 242
Db 297 gcacaaggttacgggtgagccttttagcctgcgaagtcaattgcgaagagaagttgacaa 356
QY 243 cgcctgtgatgtggaagacgtccgtcgtgaaatcacgactcactgcacttaccggaaca 302
Db 357 taaggtatgcgtagagaggttgcggaggaagtgcagatcagtcacacactggaggggca 416
QY 303 cccaaacgtgtgaaacttaagcgcacttatgaggaataacgagacccgttcattgtgat 362
Db 417 gaagacactctgcgaattgaaggggccctatgaggaataaacaacacgctgcactcgtcat 476
QY 363 ggagcttggagagaggtgagccttttggctgcgagattgtgcaagaggacattacaga 422
Db 477 ggagcttggctggcggagaactcttcacgcgatttgcagcgggggccaactacagta 536
QY 423 gcgtgcggcgtacccgtgcgagaaacgacatcgcgaagtgtgagagatgtgcactgtcaa 482
Db 537 gagggctgctcagctctatgtagaactatagtgcgaagtgttcagacgtgcactctct 596
QY 483 tggtttatgcatagagatttgaagcctgagaattcttcttgcatacaagaagagaa 542
Db 597 gggagttatgcacccgggactcgaagcccgagaatttctgtcttaacaagaagaggga 656
QY 543 tctgcacttaaggctattgatttgggttatctgttcttcttcttctcctcgaagcctggagaggtt 602
Db 657 tgcacctgaaggcagcggatttggcttcttcttcttctcctcgaagcctggagaggtt 716
QY 603 tacagagattgttgaagtccttatttatgtgcgaagttgttgaagagaaattatgg 662
Db 717 tacagatacgttggaaagtcttactacgtggcaccagaggttttgcgtgaactatgg 776
QY 663 accagaggttatgttggagtgctgagattatcctctacatcttgccttgccttgccttgcct 722
Db 777 gccagaggtctgatgttggagtgccggagtcattcttcttcttcttcttcttcttgccttgcct 836
QY 723 tccgttttggcagagactgaacaaagtgtggtccttgccttgccttgccttgccttgccttgcct 782
Db 837 tcccttctgggcagaaaccgaacaaaggtattttgagccgtaatgcacgtgcactatgga 896
QY 783 ttttaagagagatccttggctgcagatatcagagagcgcaaaagagcctgttgaagcagat 842
Db 897 tttaactagtgatccttggccttcaattctcaaaagcgcaaaagatctgtgaaagagat 956
QY 843 gttggaacctgattcaactaagcgtttgactgctcagcaagttcttgccttgccttgccttgcct 902

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Query Match 35.1%; Score 358.4; DB 22; Length 2363;
Best Local Similarity 64.7%; Pred. No. 3e-99;
Matches 533; Conservative 0; Mismatches 291; Indels 0; Gaps 0;

QY 125 agtacattcttagacgagaactcgtgcgcggaattcggaaatcagcatctcttctgtacag 184
Db 589 actacacattggggagagaactggtaggggtcaatttgggttacctactctgtgcactg 648

QY 185 atagagagactcgtgaagctttagcttgcgaatcaatctccaagagagaagctccgaaacg 244
Db 649 acaaaagactggccaaatattgcttgcgaatcaatctccaagagagaagcttgcgaac 708

QY 245 ccgtcgaatgtggaagacgctcgtgcgaatcagatcatgtcaactttacocggaacac 304
Db 709 agcgtgaataagatgatagagagagagattcagatcatgcagcatagagtgtgtaac 768

QY 305 caaacgttgaacttaagcgaacttatgagataacgagacgctgcacatcttctgtatgg 364
Db 769 ctacacatttgggaatttaaggtgcttatgagataaaacatctgtgaactcttctgtatgg 828

QY 365 agcttttgaagaggtgagcttttggctggttgcgaagagagacattatcacagac 424
Db 829 agcttgcgtgcggggaggttctgtatgagattatgtctgaagggtcattatagtgaac 888

QY 425 gtgcggcgtcgaactcgcgcgagaacatcgcggaagcttgcgaagcttgcgaagcttgcga 948
Db 889 agcgtgcctcaatctgtgagcagatgttaattgttgcgaagcttgcgaagcttgcga 1008

QY 485 gtgtatgcataagatttgaagcctgagaatttcttcttgcgaagagagagaaatt 544
Db 949 gtgtatgcataagatttgaagcctgagaatttcttcttgcgaagagagagaaatt 1008

QY 545 ctgcacttaagcttatatttctgttcttcttcttcttcttcttcttcttcttcttcttctt 604
Db 1009 ctctcttgaagccactgatttgggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1068

QY 605 cagagattgttggagctcctattatattgcctcagagagagagagagagagagagagag 1128
Db 1069 gggatagtagtagcagcttactatgtgcctcagagagagagagagagagagagagagag 1128

QY 665 cagagattgttggagctcctattatattgcctcagagagagagagagagagagagagag 1188
Db 1129 aggagattgttggagctcctattatattgcctcagagagagagagagagagagagagag 1188

QY 725 cgttttggcagagactgaacaaagcttgccttgccttgccttgccttgccttgccttgcctt 784
Db 1189 ccttttggcagagactgaacaaagcttgccttgccttgccttgccttgccttgccttgcctt 1248

QY 785 ttaagagagatccttggctgcagatcatcagagagagagagagagagagagagagagag 844
Db 1249 tcgaaagcaaaccttggccatcaatttcaaatgttgcgaagagagagagagagagagag 1308

QY 845 tggaaacctgattcaactaagcgttgccttgccttgccttgccttgccttgccttgccttgc 904
Db 1309 tgaacagggacccaagaacggttactgccttgccttgccttgccttgccttgccttgccttgc 1368

QY 905 agaatacgaagaaag 948
Db 1369 gagatgttgaagcagcagacgaagcgaatagacagctgtctgtcttc 1412

RESULT 10
AAF74278
ID AAF74278 standard; DNA; 2040 BP.
XX
AC AAF74278;
XX
DT 04-MAY-2001 (first entry)
XX
DE Rice calcium dependent protein kinase clone #2.
XX

KW Calcium dependent protein kinase; CDPK; herbicide resistance;
XX paraquat; diquat; crop production; ds.
OS Oryza sp.
XX
PN WO200107592-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-GB02876.
XX
PK 27-JUL-1999; 99GB-0017642.
XX
PA (ZENE) ZENECA LTD.
XX
PI Holt CD, White AJ, Michael AJ, Osborn RW;
XX WPI; 2001-168549/17.
DR
XX
PT Producing herbicide resistance plants by inhibiting calcium dependent
PT protein kinase in plants or by providing an intracellular vacuolar
PT transporter capable of transporting agrochemical into plant vacuole
PS Claim 18; Page 40; 50pp; English.
XX
CC The present invention describes a method of producing plants which are
CC resistant to the herbicides paraquat and diquat, involving inhibiting in
CC the plants a calcium dependent protein kinase (CDPK) and selecting those
CC plants which are resistant to the agrochemical of interest. This is
CC useful in the production of crops with herbicide resistance.
XX
SQ Sequence 2040 BP; 586 A; 415 C; 513 G; 526 T; 0 other;

Query Match 34.8%; Score 355.4; DB 22; Length 2040;
Best Local Similarity 64.6%; Pred. No. 2.3e-98;
Matches 530; Conservative 0; Mismatches 291; Indels 0; Gaps 0;

QY 127 tacatcttaggcagagaactcgtgcgcggaattcggaaatcagcatctcttctgtacagat 186
Db 425 tactcctctggaaaaggaaactcggaaaggacagtttgggtgacatcactctgtcacggag 484

QY 187 agagagactcgtgaagctttagcttgcgaatcaatctccaagagagaagctccgaacccg 246
Db 485 atcgcgtaggttgaagcagtagcttgcgaatcactctctaaagcgaagcttgcgaagc 544

QY 247 gtcgagtggaagacgttcgctgcgaatcagatcagatcagatcagatcagatcagatcag 306
Db 545 gccgacagggagagacattcgcggagagatcagatcagatcagatcagatcagatcagatcag 604

QY 307 aacgttggaaacttaaaagcgaacttatgagataacgagacgctgcacatcttctgtatggag 366
Db 605 aacattgcgaggttcgcgggagcagatagagacagagacatgcctcctgtgtatggag 664

QY 367 ctttgcgaagaggtgcagcttttgcgagattgttgcgaagagagacattatcacagagcgt 426
Db 665 cctgcgctgttggagcttgcgagattgttgcgagattgttgcgaagagagacattatcacagagcgt 724

QY 427 gcgcgctcagcgtgcgagacagcgtgcggaagttgtgcgagattgtgcagatgcagatgcag 486
Db 725 gcgcgctcagcgtgcgagagagcgtgcggaagttgtgcgagattgtgcagatgcagatgcag 784

QY 487 gttatgcataagatttgaagcctgcgaatcttcttcttcttcttcttcttcttcttcttctt 546
Db 785 gtcgagcagctgtgatttgaagcctgcgaatcttcttcttcttcttcttcttcttcttcttct 844

QY 547 gcaattgaagcatttgcgagatttgcgagatttgcgagatttgcgagatttgcgagatttgcg 606
Db 845 atgcacaaagcactgatttgcgagatttgcgagatttgcgagatttgcgagatttgcgagatttgcg 904

QY 607 gagatttgcgaagccttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 666
Db 905 gacatttgcgaagccttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 964

PR 02-AUG-1999; 99US-0146386.
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 PR 02-AUG-1999; 99US-0146389.
 PR 03-AUG-1999; 99US-0147036.
 PR 04-AUG-1999; 99US-0147204.
 PR 04-AUG-1999; 99US-0147302.
 PR 05-AUG-1999; 99US-0147192.
 PR 05-AUG-1999; 99US-0147260.
 PR 06-AUG-1999; 99US-0147303.
 PR 06-AUG-1999; 99US-0147416.
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 PR 13-AUG-1999; 99US-0148684.
 PR 16-AUG-1999; 99US-0149368.
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 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
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 PR 27-AUG-1999; 99US-0151080.
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 PR 31-AUG-1999; 99US-0151348.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
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 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
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 PR 12-OCT-1999; 99US-0158232.
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 PR 26-OCT-1999; 99US-0161360.

PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 34.7%; Score 354; DB 21; Length 1392;
 Best Local Similarity 65.9%; Pred. No. 5.le-96;
 Matches 513; Conservative 0; Mismatches 265; Indels 0; Gaps 0;

QY 133 ttaggacgagaactcgtcgcggaattcggaaatcgttatctttgtacagatagagag 192
 ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
 Db 28 ttagggaagagcgtcgcgagggccaatttggtgtcacacacctctgcacacagaagca 87
 QY 193 actcgtgaagctttagcttgcacaaatacattccaaaggaagctccgaacgcgtcgat 252
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 88 acaggtcatcaattgcttgcacagacgatgcacaaagaaagcttgaacaaaggaagac 147
 QY 253 gtggaagacgtccgctggaagtcacgacatgctcaactttacoggaacacccaaacgtt 312
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 148 attgaggatgtaagaagagaagtgacagataatgcatacttgcactggtcacaacacatt 207
 QY 313 gtgaacttaagcgcacttatggagataacgagacggtgcattctgtgtgagcttctgt 372
 ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 208 gtggagcttaaggggcttatgagataagcattccgtgcattggttatggagcttgc 267
 QY 373 gaaggagggtgagcttttggctcgattgttgaagaggacattatcacagagcgtgcggcg 432
 ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 268 gcagggtggagagtggttcgagattgttgcataagacattctctgtaaaaggacattactcggagagagcagct 327
 QY 433 gctacgcgtcggaagacgacgtcggaagttgtgagagatgtgcatgtgcatgtcattgtgtatg 492
 ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 328 gcttctgtctaagacgattgttcagattgtgcatacttgcattccatgggggtgatt 387
 QY 493 catagagattgaagcctgagaattcttctgtttgttaacaaagagagaaattctgcactt 552
 ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 388 cacagggattgaagccagagaaacttctctgtcacaacaaagatgagaattctctctc 447
 QY 553 aaggctattgatttgggttattctgtctcttctttaaaccctggagagaggtttcacagagatt 612
 ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 448 aaagctactgacttgggtgtcggttcttctcaacagccaggagaggtattcaaggatatt 507
 QY 613 gttgaagtcctattatattatgctccagaagtgttgaagagaaattatggaccagaggtt 672
 ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 508 gtggggagtgcttattacatcgcaactgaggtttgaaaagaaagtatggaccagagga 567
 QY 673 gatgtgtgagtgctggagttatctctacatctgttctgtgtgttctcgttcttgg 732
 ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 568 gatatgtggagcttgggtgtcattgtgtatctctcttctgtgtgtgtcccgscattctgg 627
 QY 733 gcagagactgaacaaaggtgtggtctcttgcattcttggagggttctgtattttaagaga 792
 ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 628 gctgagtcggagaacgagattatcaacgcaactcctggagacatgtgtgattctcaagt 687
 QY 793 gatccttggctgcagatatacagagagcgaagagccttgtgaagcagatgttggaaacct 852
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 Db 688 gatccatggccatccatctcctccaggcaaggtctgttgaagaagatgctcaactct 747
 QY 853 gattcaactaagcgtttgactgctcagcaaggttcttgcatacccttggatcagaagt 910
 ||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 748 gatccaaagcaagactaactgctgcacagttctcaaccatccatggatcaaggagg 805

RESULT 12
 AAF74271
 ID AAF74271 standard; DNA; 1723 BP.
 XX AAF74271;
 AC AAF74271;
 XX
 DT 04-MAY-2001 (first entry)
 XX
 DE Maize calcium dependent protein kinase clone #1.
 XX

PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
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PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.

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PR 29-OCT-1999; 99US-0162142.
Query Match 32.9%; Score 335.4; DB 21; Length 1671;
Best Local Similarity 63.7%; Pred. No. 2,7e-92;
Matches 510; Conservative 0; Mismatches 291; Indels 0; Gaps 0;

QY 102 taataaactcaagatcagacagacagatcatcttaggacgagaactcggcgcgcaaat 161
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 264 taagacaccaaactcgtgatcatatataccttagccgaagctaggccaagtcaatt 323
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 162 cgaatacagatctctgttacagagagacgtcgtgaagctttgagcttgcaaatcaat 221
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Db 324 tggaaacgacttatctatgtacagagatttccctcagcgcttgactacgcttgaagtcatt 383
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 222 ctccagagaagctccgaacgcgcctgatgtggaagcgcctcgtcggaagtcacgat 281
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Db 384 atccagagagattgatctctaaagaagatgttgaggatgttagaaggagattcagat 443
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QY 282 catgtcaactttaccggaacacccaaacgcttgaaacttaagcgaacttatgagataa 341
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Db 444 atgcatcatttagctggcaccgtagtatcgtgacgattaaaggagcttatgaggactc 503
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QY 342 cgagacgctgcactctgtgatgagctttgtgaagagagtgagcttttggctgagattgt 401
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QY 402 tgaagagagacattatacagagcgtgcggcgctaccgtcgcgagaacgacgcggaagt 461
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QY 462 tgtgaggaatgttcgatgtcaatgtgttatgcataagagatttgaagcctcgaaatttctt 521
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 522 gtttctaacagaaggagaattctgcacttaagcctattgatttggtttactgttct 581
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QY 582 ctttaaacctggagagagtttacagaagattgttggaagctcctattatggtccacga 641
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Db 804 ggttttgtcaaacgttatggcctgaagcgtgatgtgtgagcgtgtgtgttatattga 863
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QY 702 catcttctgtgtgttctcctcgttttgggcagagactgaaacaggtgtggtcctgc 761
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Db 924 tgtgtgaagagatatatcgcactttgagtcagacccgtggcctgtgatccgacagtcgc 983
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QY 822 aaagacgcttgtgaagcagatgttggaaacctgattcaactaagcgtttgactgcacga 881
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Db 984 taagacttgatccgcagaattgttatcctccaagcctgcagaagctttgacgcgtcatga 1043
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   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1044 agtcttgcgtcatccattggat 1064
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RESULT 14
AAAF7427;
ID AA74272 standard; DNA: 2306 BP.
XX
AC AA74272;
XX
DT 04-MAY-2001 (first entry)
XX
DE Maize calcium dependent protein kinase clone #2.
XX
```

```
KW Calcium dependent protein kinase; CDPK; herbicide resistance;
KW paraquat; diquat; crop production; ds.
XX
XX Zea mays.
XX
XX WO200107592-A2.
XX
XX 01-FEB-2001.
XX
XX 26-JUL-2000; 2000WO-GB02876.
XX
XX 27-JUL-1999; 99GB-0017642.
XX
XX (ZENE ) ZENECA LTD.
XX
XX Holt CD, White AJ, Michael AJ, Osborn RW;
XX
XX WPI; 2001-168549/17.
XX
XX Producing herbicide resistance plants by inhibiting calcium dependent
XX protein kinase in plants or by providing an intracellular vacuolar
XX transporter capable of transporting agrochemical into plant vacuole
XX
XX Claim 18; Page 35-36; 50pp; English.
XX
XX The present invention describes a method of producing plants which are
XX resistant to the herbicides paraquat and diquat, involving inhibiting in
XX the plants a calcium dependent protein kinase (CDPK) and selecting those
XX plants which are resistant to the agrochemical of interest. This is
XX useful in the production of crops with herbicide resistance.
XX
XX Sequence 2306 BP; 590 A; 519 C; 611 G; 586 T; 0 other;
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Query Match 32.6%; Score 332.8; DB 22; Length 2306;
Best Local Similarity 64.3%; Pred. No. 2e-91;
Matches 499; Conservative 0; Mismatches 277; Indels 0; Gaps 0;

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QY 307 aacgttgtgaacttaaacgcacttatgagataacgagacgcgtgcactctgtgatggag 366
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Db 845 aacatttgtgagttccggggagacacgaggaacagagaatgtccattgtgtgatggag 904
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QY 367 ctttgtgaagaggtgagctttttgtcggtattgttgcgaagagacattatcacagcgt 426
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QY 427 gcggcgctacgcgtcgcggaacgatcgcggaagtgtgaggtgtgtcatgtcaatggt 486
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Db 965 gcagctgtcaaatctgcagagcagttgtgaatgtgttcaaacatttggcacttcatgggt 1024
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 487 gttatgcatagagatttgaagcctgagaattctgtttgttcttaacacagagaagaattct 546
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Db 1025 gtgatgcacgtgacctgaacccggaaactcttctgtgcgacgaaggaggagaatgca 1084
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QY 547 gcacttaagcctattgtttgtttatctgttcttcttcttaacctgagagaggtttaca 606
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QY 607 gagatttgtggaagctccttattatgtgtccacagaagtgttgaagagaataattggacca 666
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Db 1145 gacatcgttggaagtgttattatgttgcgcctgaagtctttaaagcggagctatggaaa 1204
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QY 727 ttgtgggcagagactgaacaagggtgctgcttgcctcttgagggaggtctcttgattt 786
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  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 847 gaacctgattcaactaaagcgtttgactgctcagcaagttcttgcatacccttggat 902
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Db 1385 aacagagatccaaagaaagactgacttcagctcaagtcttcaacattcaggt 1440

RESULT 15
AAAF74273
ID AAF74273 standard; DNA; 2436 BP.
XX
AC AAF74273;
XX
DT 04-MAY-2001 (first entry)
XX
DE Soybean calcium dependent protein kinase clone #1.
XX
KW Calcium dependent protein kinase; CDPK; herbicide resistance;
KW Paraquat; diquat; crop production; ds.
XX
OS Glycine max.
XX
PN WO200107592-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-GB02876.
XX
PR 27-JUL-1999; 99GB-0017642.
XX
PA (ZENE ) ZENECA LTD.
XX
PI Holt CD, White AJ, Michael AJ, Osborn RW;
XX
RW WPI; 2001-168549/17.
XX
PS Producing herbicide resistance plants by inhibiting calcium dependent
PT protein kinase in plants or by providing an intracellular vacuolar
PT transporter capable of transporting agrochemical into plant vacuole -
XX Claim 18; Page 36-37; 50pp; English.
XX
CC The present invention describes a method of producing plants which are
CC resistant to the herbicides paraquat and diquat, involving inhibiting in
CC the plants a calcium dependent protein kinase (CDPK) and selecting those
CC plants which are resistant to the agrochemical of interest. This is
CC useful in the production of crops with herbicide resistance.
XX
SQ Sequence 2436 BP; 738 A; 435 C; 515 G; 747 T; 1 other;
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Query Match 32.2%; Score 328.8; DB 22; Length 2436;
Best Local Similarity 62.6%; Pred No. 3.4e-90;
Matches 513; Conservative 0; Mismatches 307; Indels 0; Gaps 0;

QY 128 acattttagacagagaactcgtgcgcgaattcgggaatcagtcattttgtacagata 187
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Db 739 acacacttgggaaggagtggtgtagagggcaatttgggtgacatatcttgcactgaga 798

QY 188 gagagactcgtgaactttagcttcaaatcaatccaaagagaagactccgaaccgcg 247
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Search completed: March 3, 2002, 00:39:30
Job time: 3842 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2002, 23:36:48 ; Search time 76.56 Seconds
(without alignments)
3017.340 Million cell updates/sec

Title: US-08-989-881-1
Perfect score: 1020
Sequence: 1 gttgtaaaacgacgncagt.....gcttgccgtatcatgtcat 1020

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq*
5: /cgn2_6/ptodata/1/ina/PCITUS_COMB.seq*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	226	22.2	4162	3	US-08-459-595A-26
3	226	22.2	4162	3	US-08-459-504B-26
4	226	22.2	4162	3	US-08-459-444-26
5	226	22.2	4165	1	US-07-951-715A-26
6	225.6	22.1	1349	1	US-07-951-715A-20
7	225.6	22.1	1349	2	US-08-459-448A-20
8	225.6	22.1	1349	3	US-08-459-595A-20
9	225.6	22.1	1349	3	US-08-459-504B-20
10	225.6	22.1	1349	3	US-08-459-444-20
11	219.8	21.5	2374	4	US-09-347-801-3
12	148.2	14.5	1400	1	US-08-464-164-1
13	148.2	14.5	1400	1	US-08-338-057-1
14	148.2	14.5	1400	2	US-08-668-416-1
15	136.6	13.4	1776	3	US-08-655-352-10
16	117	11.5	2514	3	US-08-655-352-1
17	97.4	9.5	498	4	US-09-347-801-7
18	84.6	8.3	5707	2	US-08-472-809B-8
19	83	8.1	270	1	US-08-181-629A-12
20	82.4	8.1	1282	2	US-08-878-989-12
21	82.4	8.1	1282	4	US-09-272-796-12
22	82	8.0	2027	3	US-08-930-996A-6
23	82	8.0	3198	4	US-08-842-306B-48
24	82	8.0	3198	4	US-08-838-973B-48
25	82	8.0	6345	2	US-08-472-809B-7
26	81.4	8.0	329	1	US-08-703-809-9
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C 31	81.4	8.0	329	3	US-09-265-628-9	Sequence 9, Appli
C 32	81.4	8.0	329	4	US-09-532-803-3	Sequence 3, Appli
C 33	81.2	8.0	4164	1	US-08-204-675-1	Sequence 1, Appli
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C 35	81.2	8.0	4164	2	US-08-796-364-1	Sequence 1, Appli
C 36	81.2	8.0	4164	5	PCT-US95-02520-1	Sequence 1, Appli
C 37	81.2	8.0	4933	1	US-08-204-675-2	Sequence 1, Appli
C 38	81.2	8.0	4933	2	US-08-660-754-2	Sequence 2, Appli
C 39	81.2	8.0	4933	2	US-08-796-364-2	Sequence 2, Appli
C 40	81.2	8.0	4933	5	PCT-US95-02520-2	Sequence 2, Appli
C 41	79.8	7.6	11233	4	US-08-980-832-27	Sequence 27, Appli
C 42	77.4	7.6	380	2	US-08-735-609-5	Sequence 5, Appli
C 43	77.4	7.6	380	2	US-08-735-609-5	Sequence 5, Appli
C 44	77.4	7.6	380	3	US-03-315-372-5	Sequence 5, Appli
C 45	77.4	7.6	380	3	US-09-244-752-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-459-448A-26
; Sequence 26, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5859336artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,448A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403

```
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-9582
TELEFAX: (919)541-8689
- INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
FEATURE:
NAME/KEY: exon
LOCATION: 2691..2804
FEATURE:
NAME/KEY: intron
LOCATION: 2805..2906
FEATURE:
NAME/KEY: exon
LOCATION: 2907..3075
FEATURE:
NAME/KEY: intron
LOCATION: 3076..3177
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NAME/KEY: exon
LOCATION: 3178..3304
FEATURE:
NAME/KEY: intron
LOCATION: 3305..3398
FEATURE:
NAME/KEY: exon
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NAME/KEY: promoter
LOCATION: 1..1477
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /partial
OTHER INFORMATION: /function= "pollen-specific promoter region"
OTHER INFORMATION: /evidence= EXPERIMENTAL
US-08-459-448A-26

Query Match 22.2%; Score 226; DB 2; Length 4162;
Best Local Similarity 60.4%; Pred. No. 5.1e-61;
Matches 373; Conservative 0; Mismatches 245; Indels 0; Gaps 0;

QY 119 gqacaaagtacattcttagacgagaaactcggtcgccggaatttcggaatcagatattcttt 178
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QY 179 gtacagatagagagactcgtgaagcttttagcttgcaaatcaatctccaagagaaaagctcc 238
Db 1809 GCACGACCGGAGCGGCGGAGAACTGCGTGAAGACGATCGGAAAGCGGAAGCTGG 1868
QY 239 gaaccgctcgatgtggaagacgtcggtgaagtcaagcatcatgtcaactttaccgg 298
Db 1869 CGGCCAGGAGGACGTGGACGAGTGGGGGGAGGTGAGATCATGACCACTCTCCG 1928
QY 299 aacacccaaacgttgtgaacactaaagcgacttatgagataaacgagacgtgcatcttg 358
Db 1929 GCAGGCCAACGTGTGGCTCCGGGGCGGCTACGAGGACAAAGACAGAGCGTGCACCTCG 1988
QY 359 tgatggagctttggaagaggtgagctttttgttcggattgtggaagagagacattata 418
Db 1989 TCAITGAGCTGTGCGCGGGGAGGTCTCTGACGCGATCATGCGCCGGGGGCGAGTACA 2048
QY 419 cagagcgtgcggtaccgttcgcgagaaacgacatcgcggaagtgtgaggaagtgtcatg 478
Db 2049 CGGAGCGCGCGCGGAGCTGCTCGCGCCATCGTGCAGATCGTGCACACTGCCACT 2108
QY 479 tcaatggtttatgcatagagatttgaagcctgagaatttcttggtaacaagaagg 538
Db 2109 CCATGGGGTGTGATGACCGGGACATCAAGCGGAGAACTTCCTGTCTCAGCAAGGAGC 2168
QY 539 aqaattctgacctaaagctattgattgtttgttttattcttctttaaactggagaga 598
Db 2169 AGGACGCGCGCTCAAGGCCACCGACTTCGGCTCTTCGCTCTTCAAGGAGGGGAGC 2228
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Db 2229 TGCTCAGGGACATCGTCCGAGCGGCTACTACATCGCGCGCGGAGTGTCTCAGAGGAAGT 2288
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Db 2349 TGCTCTCTCTTGGGCGAG 2366

RESULT 2
US-08-459-595A-26
; Sequence 26, Application US/08459595A
; Patent No. 6018104
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSED: No. 6018104artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; STREET: Rd., POB 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,595A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1418..1427
OTHER INFORMATION: /note="start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
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NAME/KEY: intron
LOCATION: 3499..3713
FEATURE:
NAME/KEY: exon
LOCATION: 3714..3811

FEATURE:
NAME/KEY: promoter
LOCATION: 1..1477
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /partial
OTHER INFORMATION: /function="pollen-specific promoter region"
OTHER INFORMATION: /evidence= EXPERIMENTAL
US-08-459-595A-26
Query Match 22.2%; Score 226; DB 3; Length 4162;
Best Local Similarity 60.4%; Pred. No. 5.1e-61;
Matches 373; Conservative 0; Mismatches 245; Indels 0; Gaps 0;
QY 119 gcacacaggtacattcttaggacgagaaactcgctgcgcgcgaatcgcgaatcacgtatattt 178
Db 1749 GCGCGACCTACTGATGGGCAAGAGAGCTCGGGCGGGCAGTTCGGCGTGCACCTGT 1808
QY 179 gtacagatagagagactcgtgaagcttttagcttgcaaatcaattccaaagagaagctcc 238
Db 1809 GCACGACCGGACGAGCGGCGAGAAGCTGCGTGCAGAGCATGCGGCAAGCGGAAGCTGG 1868
QY 239 gaaccgctcgatgtggaagacgtcgctgctgaagtcaagtcacatcatctcaacttaccgg 298
Db 1869 CGGCCAGGGAGAGCTGGACGACGTGCGGCGGGAGGTGCAGATCATGCCACCTCTCCG 1928
QY 299 aacacccaaactgtgtgaaacttaaaagcgacttatagggaalaaacgagacogtgcatttg 358
Db 1929 GCCAGCCCAACGTTGGTGGGCTCCGGCGCGGTACGAGGACAAAGCAGAGGCTGCACCTCG 1988
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Db 1989 TCAITGAGCTGTGCGCGGGGGAGGCTCTTCGACCGCATCATCGCCCGGGGCCAGTACA 2048
QY 419 cagagcgtgcgcgtaccgtgcgagaaacgatcgcggaagtgtgagagatgtgcattg 478
Db 2049 CGAGGCGGGCGCGGGAGCTGCTGGGCCCATCTGTCAGATCGTGCACCTGCCACT 2108
QY 479 tcaatgggttatgcataagatttgaagcctgagaaattttctgttgcataaagaag 538
Db 2109 CCATGGGGTGTGCACCGGGACATCAAGCCCGAGAACTTCCTGCTGCTCAGCAAGGACG 2168
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Db 2169 AGGACGCGCGCTCAAGGCCACCGACTTCGGGCTCTCCGCTCTTCTTCAAGGAGGGGAGC 2228
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Db 2289 ACGGCCCGGAGCGGCACATCTGGAGGTGCGGCTCATGTCTACATCTTCTCTCGCGGGCG 2348
QY 719 ttcttcggtttggcgag 736
Db 2349 TGCTTCTCTCTGCGGACG 2366
RESULT 3
US-08-459-504B-26
Sequence 26, Application US/08459504B
Patent No. 6075185
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlino, Ellis J.


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: Sequence 26, Application US/0845944A
: Patent No. 6121014
: GENERAL INFORMATION:
: APPLICANT: Koziel, Michael G.
:           Desai, Nalini M.
:           Lewis, Kelly S.
:           Kramer, Vance C.
:           Warren, Gregory W.
:           Evola, Stephen V.
:           Crossland, Lyle D.
:           Wright, Martha S.
:           Merlin, Ellis J.
:           Launis, Karen L.
: TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
:                     NUCLEIC ACID CODING SEQUENCE
:
: NUMBER OF SEQUENCES: 94
: CORRESPONDENCE ADDRESS:
:   ADDRESS: No. 6121014artis Agribusiness Biotechnology Research, Inc.
:   STREET: 3054 Cornwallis Road
:   CITY: Research Triangle Park
:   STATE: NC
:   COUNTRY: USA
:   ZIP: 27709
:
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: IBM PC compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: PatentIn Release #1.0, Version #1.30
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/08/459,444A
:     FILING DATE: 02-Jun-1995
:     CLASSIFICATION: <Unknown>
:   PRIOR APPLICATION DATA:
:     APPLICATION NUMBER: US 07/951,715
:     FILING DATE: 25-SEP-1992
:     APPLICATION NUMBER: US 07/772,027
:     FILING DATE: 04-OCT-1991
:   ATTORNEY/AGENT INFORMATION:
:     NAME: Meigs, J. Timothy
:     REGISTRATION NUMBER: 38,241
:     REFERENCE/DOCKET NUMBER: S-18805/PI/CGC1577/CIP/DIV6
:   TELECOMMUNICATION INFORMATION:
:     TELEPHONE: (919)541-8587
:     TELEFAX: (919)541-8689
:
: INFORMATION FOR SEQ ID NO: 26:
:   SEQUENCE CHARACTERISTICS:
:     LENGTH: 4162 base pairs
:     TYPE: nucleic acid
:     STRANDEDNESS: single
:     TOPOLOGY: linear
:     MOLECULE TYPE: DNA (genomic)
:     HYPOTHETICAL: NO
:     FEATURE:
:       NAME/KEY: misc_feature
:       LOCATION: 1418..1427
:       OTHER INFORMATION: /note= "start of mRNA"
:
:   FEATURE:
:     NAME/KEY: exon
:     LOCATION: 1481..2366
:     FEATURE:
:       NAME/KEY: intron
:       LOCATION: 2367..2451
:     FEATURE:
:       NAME/KEY: exon
:       LOCATION: 2452..2602
:     FEATURE:
:       NAME/KEY: intron
:       LOCATION: 2603..2690
:     FEATURE:
:       NAME/KEY: exon
:       LOCATION: 2691..2804
:     FEATURE:
:       NAME/KEY: intron

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LOCATION: 2450..2602

;; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
;; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
;; NUMBER OF SEQUENCES: 94
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: No. 5859336artis Corporation
;; STREET: Patent & Trademark Dept., 520 White Plains
;; STREET: Rd., POB 2005
;; CITY: Tarrytown
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10591-9005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/459,448A
;; FILING DATE: 02-JUN-1995
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/951,715
;; FILING DATE: 25-SEP-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/772,027
;; FILING DATE: 04-OCT-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Pace, Gary M.
;; REGISTRATION NUMBER: 40403
;; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (919)541-8582
;; TELEFAX: (919)541-8689
;; INFORMATION FOR SEQ ID NO: 20:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1349 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHEetical: NO
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 3..1226
;; OTHER INFORMATION: /note= "cDNA sequence for maize
;; OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as
;; OTHER INFORMATION: disclosed in Figure 30."
;; US-08-459-448A-20

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Best Local Similarity 60.1%; Pred. No. 3.9e-61;
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QY 339 taacgagacgctgcatcttggatgagcttggatgagaggtgagctttttggtcgat 398
Db 65 CAAGCAGAGGGTGCACCTCGTCATGAGCTGTGCGGGGGGGGAGCTCTTCGACCGCAT 124
QY 399 tgtgaaagagacattatatacagagcgtgcggcggtaccgtgcgagaaacatcgqga 458
Db 125 CATCGCCCGGGGCGAGTACACGAGGCGCGCGCGGAGCTGCTGCGCGCCATCTGCA 184
QY 459 agttgagagatgtgcatgtcaatggtgttatgcatagagatttaagcctgagaattt 518
Db 185 GATCGTGACACCTGCACCTCCATGGGGGTGATGCAACCGGAGCATCAAGCCGAGAACTT 244
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Db 245 CTTGCTGCTCAGCAAGACGAGACCGCGGCTCAAGGGCCACCGACTTCGGGCTCTCCGT 304

QY 579 tctotttaaacctggagagaggttttaagagagattgttggagagcttattattatgctcc 638
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QY 699 ctacatcttgcttgggtgttctccgttttgggagagagactgaacaaggtgtggtct 758
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Db 605 CCAGTGCTCAATCACCCATGGAT 628

RESULT 8
US-08-459-595A-20
; Sequence 20, Application US/08459595A
; Patent No. 6018104
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6018104artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; STREET: Rd., POB 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,595A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991

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ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1349 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..1226
; OTHER INFORMATION: /note= "cDNA sequence for maize
; OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as
; OTHER INFORMATION: disclosed in Figure 30."
; US-08-459-595A-20

Query Match 22.1%; Score 225.6; DB 3; Length 1349;
Best Local Similarity 60.1%; Pred. No. 3.9e-61; Mismatches 249; Indels 0; Gaps 0;
Matches 375; Conservative 0;

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Dd ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
125 CATCGCCGCGGGCCAGTACACGGAGCGCGCGCGCGGAGCTGCTGCGCGCATCGTGA 184

QY 459 agttgtgagatgtgtcatgtcaatgtgtgtatgtagagatttgaagcctgagaattt 518
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185 GATCGTGCACACCTGCCACCTCCATGCGGGGTGATGCACCGGACATCAAGCCGAGAACTT 244

QY 519 ctgtttgtctaaagaagaggaattctgcacttaagctattgattttggtttatgt 578
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425 CTACATCTTCTCGCGCGCGTCTCCCTCTCTGGGCGAGAACGAGAACGCGCATCTTAC 484

QY 759 tgcatttgaaggaggtttctgtattttaagagagatccttggctgcagatatcagagag 818
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QY 819 cgcacaagacgttgtgaagcagatgttgaacctgtatcaactaagcgtttgactgtca 878
Dd ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
545 AGCCAAGGATCTCGTCAAGAAGATGCTCAACATCAACCCCAAGGAGCGGCTCAGCGGTT 604

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Query Match

22.1%; Score 225.6; DB 3; Length 1349;

Best Local Similarity 60.1%; Pred. No. 3.9e-61;
Matches 375; Conservative 0; Mismatches 249; Indels 0; Gaps 0;

QY 279 gatcatgtcaactttaccggaacaccccaacggtgtgaaacttaaaagcagcttatgaga 338
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Db 5 GATCATGCCACCACTCTCCGCCACCCCAACGCTGTGGCTCCGCCGCGGTACGAGGA 64

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QY 399 tgttgaagagagacattatcacagagctgagcggtaccgtcgcgagaacgatogga 458
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Db 145 CATGCCCGGGCGGACGTACAGGAGCGGGCGCGCGGAGCTGTGGCGGCATCGTGCA 184

QY 449 agttgaggatgtgtcatgtcaatggtgttatcatagagatttgaagcctgagaattt 518
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Db 185 GATCGTGACACCTGCCACTCCATGGGGGTGATGCACCGGACATCAAGCCCGGAACTT 244

QY 519 ctgtttgttaacagaagaagaatttctgcacttaaggctattgatttggtttctgt 578
|||||
Db 245 CCTGCTGCTCAGCAAGGAGGAGGACGCGCGGCTCAAGGCGCACCGACTTCGGCTCTCCGT 304

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Db 305 CTCTTCAAGGAGGCGGAGCTGCTCAGGACATCGTCGCGAGCGGCTACTATACGCGCC 364

QY 639 agaagtttgaagagaaattatggaccagaggttggatgtgtgagtgctggagttatct 698
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Db 365 CGAGGTGCTCAAGAGGAGTACGCGCGCGGAGCGCCGACATCTGGAGCGCTCGGCTCATGT 424

QY 699 ctacatcttctgtgtgttcttcctgttttggcgagagactgaacaaaggtgtgctct 758
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Db 425 CTACATCTCTCCGCGCGGCTGCTTCTCTGGCAGAGAACGAGAACGCGCATCTTCAC 484

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Db 485 CGCATCTCTCGAGGCGAGCTTACCTCTCCAGCGGCCATGTCACACATCTCGCGGG 544

QY 819 cgcaagagccttgaagcagatgttggacacctgattcaactaaagcgtttgactctca 878
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Db 545 AGCCAAGGATCTGCTCAAGAGAGATGCTCAACATCAACCCCAAGGAGCGGCTCAGCGGTT 604

QY 879 gcaagtttggatcacaccttgat 902
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Db 605 CCAGGTCTCAATCAACCCATGGAT 628

RESULT 10

US-08-459-444-20

Sequence 0, Application US/08459444A

Patent No. 6121014

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.

Desai, Nalini M.

Lewis, Kelly S.

Kramer, Vance C.

Warren, Gregory W.

Evola, Stephen V.

Crossland, Lyle D.

Wright, Martha S.

Merlin, Ellis J.

Launis, Karen L.

TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED

NUCLEIC ACID CODING SEQUENCE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESS: No. 6121014artis Agribusiness Biotechnology Research, Inc.

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8889
INFORMATION FOR SEQ ID NO: /note= "cdna sequence for maize
pollen-specific calcium dependent protein kinase gen.
disclosed in Figure 30."

SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
FEATURE:

NAME/KEY: CDS
LOCATION: 3..1226
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-08-459-444-20

Query Match

22.1%; Score 225.6; DB 3; Length 1349;

Best Local Similarity 60.1%; Pred. No. 3.9e-61;

Matches 375; Conservative 0; Mismatches 249; Indels 0; Gaps 0;

QY 279 gatcatgtcaactttaccggaacaccccaacggtgtgaaacttaaaagcagcttatgaga 338
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Db 5 GATCATGCCACCACTCTCCGCCACCCCAACGCTGTGGCTCCGCCGCGGTACGAGGA 64

QY 339 taacagagaccgtgacatttggatggaagctttgtgaagaggtgagcttttggctggat 398
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Db 65 CAAGCAGAGCGTGCACCTCGTCATGGAGCTGTGGCGGGGAGGCTCTTCACCGCAT 124

QY 399 tgttgaagagagacattatcacagagcgtgagcggtaccgtcgcgagaacgatcgga 458
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Db 125 CATGCCCGGGCGGACGTACAGGAGCGGGCGCGGAGCTGTGGCGGCATCGTGCA 184

QY 459 agttgaggatgtgtcatgtcaatggtgttatcatagagatttgaagctcttatatatgctcc 518
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Db 185 GATCGTGACACCTGCCACTCCATGGGGGTGATGCACCGGACATCAAGCCCGGAACTT 244

QY 519 ctgtttgttaacagaagaagaatttctgcacttaaggctattgatttggtttctgt 578
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Db 245 CCTGCTGCTCAGCAAGGAGGAGGACGCGCGGCTCAAGGCGCACCGACTTCGGCTCTCCGT 304

QY 579 tctctttaaacctgagagaggtttacagagattgttgaagctcttatatatgctcc 638
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Db 305 CTCTTCAAGGAGGCGGAGCTGCTCAGGACATCGTCGCGAGCGGCTACTATACGCGCC 364

QY 639 agaagtttgaagagaaattatggaccagaggttggatgtgtgagtgctggagttatct 698
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Db 365 CGAGGTGCTCAAGAGGAGTACGCGCGCGGAGCGCCGACATCTGGAGCGCTCGGCTCATGT 424

QY 699 ctacatcttctgtgtgttcttcctgttttggcgagagactgaacaaaggtgtgctct 758
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Db 425 CTACATCTCTCCGCGCGGCTGCTTCTCTGGCAGAGAACGAGAACGCGCATCTTCAC 484

QY 759 tgcatttgaagggagttcttatttgaatttaagagagagatccttggctgcagatatcagagag 818
Db 485 CGCATTCTCGAGGGGAGAGCTTACCTCTCCAGGAGCCATGCGCACACATCTCGCGGG 544
QY 819 cgcagaagccttgaagcagagattgttggaacctgattcaactaagcgtttgactgctca 878
Db 545 AGCCAAGGATCTGTCAGAGAGATGCTCACATCACCCCAAGAGGCGGCTCACGGCGTT 604
QY 879 gcaagttcttgatcaaccttggat 902
Db 605 CCAGGCTCTCAATCACCCATGGAT 628
RESULT 11
US-09-347-801-3
; Sequence 3, Application US/09347801
; Patent No. 6262345
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/347,801
; EARLIER FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,438
; EARLIER FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 2374
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-347-801-3

Query Match 21.5%; Score 219.8; DB 4; Length 2374;
Best Local Similarity 57.4%; Pred. No. 3.4e-59;
Matches 417; Conservative 0; Mismatches 307; Indels 3; Gaps 1;
QY 206 tagcttgcaaatcaatctccaagagagaagctccgaaccccgctcgatgtggaagacgtcc 265
Db 796 tcgcgtcaagatcatcgcaagctcaagatgacaacggaatcatccattgaggatgttc 855
QY 266 gtccgtgaagtcacatgctcaatttaccggaacaccccaacgcttggaacctaaag 325
Db 856 gtagaagaataaattttgagagcgttatccgggacaaataatctcgcaaatctatg 915
QY 326 cgacttatgagagataacgagaccgtgcatcttctgtaggagcttttgaaggaggtgagc 385
Db 916 atgcattgagagatggcctcaatgctctacatgtcatggaattatgtgaggaggagaat 975
QY 386 ttttggctgagattgttgaaga---ggacattatacagagcgtgcggcggtaccgtcg 442
Db 975 tctagacagaattatgacagagcgggagatacacagaggaagatgccaaagcagtg 1035
QY 443 cgagaacgtcggaagtgtgagatgtgcattgctcaatggtttatgcataagatt 502
Db 1035 ttgtacagattttgagcgtagtagctcttctcattcctcagggtgtgctcattgatt 1095
QY 503 tgaagcctgagaattcttctgttgaacaagaagagagattctgcactaaaggtattg 562
Db 1096 tgaagcagagaattctccttttccaaacaggagatgaaatgctcccatgaagtgattg 1155
QY 563 atttgggttactgtctcttctttaaaccctggagaggtttacagagattgttgaagtc 622
Db 1156 atttgggtctctgtattctcattagaccagatgaaagccttaattatgtattgtgaagt 1215
QY 623 ctattatgctccagaaggttgaagagaataattatggaccagaggttgatgtgtgga 682
Db 1216 catattatgtgccacagaggtttcacacagatcatatgattggaagcagacatttga 1275
QY 683 gtgctggattatctctacatctgtcttgggttctcctcgttttggggcagagactg 742

Db 1276 gtataggtgataaagctacattctctgtgagcagtcgccaattctgggcaagaacag 1335
QY 743 aacaaggtgtggtcttgcattcttgcattcttgcagggaggttcttgaatttaagagagatccttgg 802
Db 1336 aatcaggaattatccgactctgtgtgagagctgataccaaactttgattgattcaaccgtggc 1395
QY 803 cgcagatatcagagagcgcgaagacccctgtgaagcagatgttgggaacctgattcaacta 862
Db 1396 ctacagtatcagctgaagctaaagattttgtgaagagatttctgaacaagagattaccgcga 1455
QY 863 agcgtttgactgtcagcaagcttctgatacccttggatcacaccttggatcacagaatgcaaaaaagga 922
Db 1456 aaagaatgacctgtttcaagcactgactcactctgtgtgctgagatgaacaaagcaga 1515
QY 923 tcaagct 929
Db 1516 tcccgct 1522
RESULT 12
US-08-464-164-1
; Sequence 1, Application US/08464164
; Patent No. 5614195
; GENERAL INFORMATION:
; APPLICANT: Tomley, Fiona M.
; APPLICANT: Dunn, Paul P. J.
; APPLICANT: Bumstead, Janene M.
; APPLICANT: Vermeulen, Arno N.
; TITLE OF INVENTION: Coccidiosis poultry vaccine
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 5614195el Patent Department
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: us/08/464,164
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELEPHONE: (301) 258-5200
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1400 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: C-terminal
; ORIGINAL SOURCE:
; ORGANISM: Eimeria maxima
; STRAIN: Houghton
; DEVELOPMENTAL STAGE: sporozoite
; IMMEDIATE SOURCE:
; LIBRARY: sporozoite cDNA cloned in Lambda ZAPII
; CLONE: Em70-1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1368
; US-08-464-164-1

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Query Match      14.5%; Score 148.2; DB 1; Length 1400;
Best Local Similarity 52.5%; Pred. No. 8.3e-37;
Matches 324; Conservative 0; Mismatches 293; Indels 0; Gaps 0;

QY 298 gaacacccaaacgtgtgaaacttaagcgacttatgagataaacgagaccgtgcacttt 357
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Db 151 GATCATCTTAATATCATGAAATATATGAATCTTTGAGGATAAAGGATATCTTTATCTT 210

QY 358 gtatgagagcttggtaagagaggtgagcttttggcgagttgtgcaagagacattat 417
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 211 GTTACAGAAATATATACAGGAGGAGAAATTTTCAATGAAATTTAATCGAAAAAGATTC 270

QY 418 acagagcggtcgcggtgctacgtcgagagaaacatcggaagtgtgagagatgtcat 477
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 271 AGCGAGCGGATCGAGCTCGTATAGTACGTCAGGTTCTATCGGTTAATAATTATATGCAT 330

QY 478 gtcaatggtgttatgcatagagatttgaagcctgagacgttgcatacaagaag 537
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 331 CGTAATAAAATAGTTTCATAGAGATTTAAAGCCAGAGAAATTTATATAGAGATAAAAA 390

QY 538 gagaattctgcacttaaggctattgatttggtttttttttttttttttttttttttt 597
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 391 AAAGATGCAAAATATACGAATTTATGTTTGGGTTTATACACATTTTTCAGCCCCAAAA 450

QY 598 aggtttacagagattgttggagcttcttatttatatggtccacgaagctgttgaagagaaat 657
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 451 AAAATGAAGATAAAAATCGGACCGGCTACTACATTCGCCCTGAGGTGTCGACGGAACA 510

QY 658 tatgaccagaggttggatgtgtggagtgctgagttatctctacattcttctgttgtgt 717
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 511 TAGCATGAGAAATGCGACGCTGCTGGTCTACGGGTGTTTATCTCTATATCTCTCTGTGT 570

QY 718 gtctccgttttggcgagagactgaacaggtgtggtctgtgcaatcttggagggagtt 777
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 571 TGTCTCCATTTACGCGGAGCAATGAATTTGAAATTTCTAAAGAAAGTCGAGAAAGGAAAA 630

QY 778 cttgattttaagagagatccttggcgagatcatgagagcgcaagagccttggagag 837
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 631 TTCACCTTCGATTTACACAGTGGCGTAGGTTAGCGAGCCACCAAGAAATTTAATTAGG 690

QY 838 cagatattggaacctgattcaactaagcgtttgactgctcagcaagcttcttgatccct 897
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 691 AGATGTTTACATATGATCCCTCAATCGCTATATACGAAAGATGCAATGATATCAATCA 950

QY 898 tggatacagaatgcaaa 914
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Db 751 TGGATAAAAGTACAGA 767

RESULT 13
US-08-338-057-1
; Sequence 1, Application US/08338057
; Patent No. 5795741
; GENERAL INFORMATION:
; APPLICANT: Tomley, Fiona M.
; APPLICANT: Dunn, Paul P. J.
; APPLICANT: Bumstead, Janene M.
; APPLICANT: Vermeulen, Arno N.
; TITLE OF INVENTION: Coccidiosis poultry vaccine
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Organon Teknika Corporation
; STREET: 1330 Piccard Drive
; CITY: Rockville
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: EP 93.309078.9
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 258-5200
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1400 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: C-terminal
; ORIGINAL SOURCE:
; ORGANISM: Eimeria maxima
; STRAIN: Houghton
; DEVELOPMENTAL STAGE: sporozoite
; IMMEDIATE SOURCE:
; LIBRARY: sporozoite cDNA cloned in Lambda ZAPII
; CLONE: Em70-1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1368
; US-08-338-057-1
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Query Match      14.5%; Score 148.2; DB 1; Length 1400;
Best Local Similarity 52.5%; Pred. No. 8.3e-37;
Matches 324; Conservative 0; Mismatches 293; Indels 0; Gaps 0;

QY 298 gaacacccaaacgtgtgaaacttaagcgacttatgagataaacgagaccgtgcacttt 357
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 151 GATCATCTTAATATCATGAAATATATGAATCTTTGAGGATAAAGGATATCTTTATCTT 210

QY 358 gtatgagagcttggtaagagaggtgagccttttggcgagttgtgcaagagagacattat 417
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 211 GTTACAGAAATATATACAGGAGGAGAAATTTTGAATGAAATTTAATCGAAAAAGATTC 270

QY 418 acagagcggtcgcggtgctacgtcgagagaaacatcggaagtgtgagagatgtcat 477
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 271 AGCGAGCGGATCGAGCTCGTATAGTACGTCAGGTTCTATCGGTTAATAATTATATGCAT 330

QY 478 gtcaatggtgttatgcatagagatttgaagcctgagacgttgcatacaagaag 537
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 331 CGTAATAAAATAGTTTCATAGAGATTTAAAGCCAGAGAAATTTATATAGAGATAAAAA 390

QY 538 gagaattctgcacttaaggctattgatttggtttttttttttttttttttttttttt 597
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 391 AAAGATGCAAAATATACGAATTTATGTTTGGGTTTATACACATTTTTCAGCCCCAAAA 450

QY 598 aggtttacagagattgttggagcttcttatttatatggtccacgaagctgttgaagagaaat 657
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 451 AAAATGAAGATAAAAATCGGACCGGCTACTACATTCGCCCTGAGGTGTCGACGGAACA 510

QY 658 tatgaccagaggttggatgtgtggagtgctgagttatctctacattcttctgttgtgt 717
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Db 511 TAGCATGAGAAATGCGACGCTGCTGGTCTACGGGTGTTTATCTCTATATCTCTCTGTGT 570

QY 718 gtctccgttttggcgagagactgaacaggtgtggtctgtgcaatcttggagggagtt 777
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 571 TGTCTCCATTTACGCGGAGCAATGAATTTGAAATTTCTAAAGAAAGTCGAGAAAGGAAAA 630

QY 778 cttgattttaagagagatccttggcgagatcatgagagcgcaagagccttggagag 837
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Db 631 TCCACCTTCGATTTCACCAAGTGGCGTAAGGTACCGAGCCAGCAAAAGATTAAATPAGG 690
QY 838 cagatgttggaacotggttcaactaagcggttgactgtcagcaagttcttgatcacocct 897
Db 691 AAGATGTTAGCATATGTCACCTCAATCGTATATCAGCAAAAGATGCATTAGATCATCCA 750
QY 898 tggatacagaatgcaaa 914
Db 751 TGGATAAAAAGTACAGA 767

RESULT 14
US-08-668-416-1
; Sequence 1, Application US/08668416
; Patent No. 5845722
; GENERAL INFORMATION:
; APPLICANT: Tomley, Fiona M.
; APPLICANT: Dunn, Paul P. J.
; APPLICANT: Bumstead, Janene M.
; APPLICANT: Vermeulen, Arno N.
; TITLE OF INVENTION: Coccidiosis poultry vaccine
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 5843722el Patent Department
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/668,416
; FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA: US/08/464,164
; APPLICATION NUMBER: US/08/464,164
; FILING DATE: June 2, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 258-5200
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1400 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: C-terminal
; ORIGINAL SOURCE:
; ORGANISM: Eimeria maxima
; STRAIN: Houghton
; DEVELOPMENTAL STAGE: sporozoite
; IMMEDIATE SOURCE:
; LIBRARY: sporozoite cDNA cloned in Lambda ZAPII
; CLONE: Em70-1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1368
US-08-668-416-1

Query Match 14.5%; Score 148.2; DB 2; Length 1400;
Best Local Similarity 52.5%; Pred. No. 8.3e-37;
Matches 324; Conservative 0; Mismatches 293; Indels 0; Gaps 0;

QY 298 gaacacccaaacgctgtgaacactaaagcgacttatgaggataaagacagacgctgcatt 357
Db 151 GATCATCCTAATATCATGAATATATGAATCTTTGAGGATAAAGGATACTTTTATCTT 210
QY 358 gtgatggactgttggaaggagggtgagotttttgtgcgagttgttgcgaaggagacattat 417
Db 211 GTTACAGAAAGTATATACAGGAGGAGAAATTATTGTATGAATTTATTAAATCGAAAAAGATTC 270
QY 418 acagagcgtcgcggtaccgtcgcgagaaacgacgcggaagttgtgaagatgtgcat 477
Db 271 AGCGAGCGGATGAGCTCGTATAGTAGTACGTGAGGTCTATCGGGTATAAATATATGAT 330
QY 478 gtcaatggtgttatgcataagatttggaagcctgagaatttctgtgttgcacaagaag 537
Db 331 CGTAATAAAATAGTTCATAGAGATTAAAGCCAGAGAAATTTATTATAGAGAAATAAAAA 390
QY 538 gagaattctgcacttaaggctattgatttggtttatctgttctctttaaaccctggagag 597
Db 391 AAAGATGCAAAATATACGAATTTATTGTTGGTTATCTACACATTTTGAGCCCAAAAA 450
QY 598 aggtttacagagattgttgaagtccttatttatatgctccagaggtgtgaagagaat 657
Db 451 AAATGAGAGATAAAATCGGACCGCTACTACATTGCCCTGAGGTGCTGCACGGGAACA 510
QY 658 tatggaccagaggtgtgtgtgagtgctgagtgcttctacatcttctgttctgtt 717
Db 511 TACGATGAGAAATGCGACGCTGCTCTACGGGTCTTATCCTCTATATCCTTCTCTCGGT 570
QY 718 gtctcctgtttggcgagagactgaacaagggtgtgctcttgcacatcttgaggggagtt 777
Db 571 TGICCTCCATTTAACGGAGCAATGAAATTTGAAATTTAAAGAAAGTCGAGAAAGGAAAA 630
QY 778 cttagattttaagagagatccttgcagatatccagagagcgaagagccttctgtgaag 837
Db 631 TTCACCTTCGATTTACCCACAGTGGCGTAAGGTTAGCCAGCCAGCAAGATTTAAATAGG 690
QY 838 cagatgttgaacctgattcaactaagcgtttgactgtcagcaagttcttgatcacocct 897
Db 691 AAGATGTTAGCATATGTACCTCAATCGTATATCAGCAAAAGATGCATTAGATCATCCA 750
QY 898 tggatacagaatgcaaa 914
Db 751 TGGATAAAAAGTACAGA 767

RESULT 15
US-08-655-352-10
; Sequence 10, Application US/08655352
; Patent No. 6077991
; GENERAL INFORMATION:
; APPLICANT: Bachettira W. Poovaiiah, Zhihua Liu,
; APPLICANT: Shameekumar Patil, Daisuke Takezawa
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESS: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,352

Db 885 CTGCTCAAGAGATACTTGACATCCATGGGT 915

Search completed: March 3, 2002, 01:28:57
Job time: 6729 sec

Query Match 13.4%; Score 136.6; DB 3; Length 1776;
Best Local Similarity 52.1%; Pred. No. 4.1e-33;
Matches 329; Conservative 0; Mismatches 299; Indels 3; Gaps 1;

QY 275 tcacgatcatgtcaactttaccggaacacccaaactgttgaaacttaaacgacacttatg 334
Db 285 TTAAGATCGTGAAGATGTTCTCCTCATCTCAACGTCATTCATCTCTACGACGTTTGTG 344

QY 335 agataaacgagacgctgtcatctgtgatgagctttgtgaagaggtgagctttttgttc 394
Db 345 AGGATCCTTCTGGAGTTCATCTCATTTTGGAGCTTTGCTCTGCTGCTGAGCTCTTTGATC 404

QY 395 ggattgttgcaagaggacattatacagagcggtgcggcggtcacgtgcgcgagaaacgacgtg 454
Db 405 GGATTGCTGGGCAAGCAGAGATTAATGAGGCTGGGGGCTGCTGCTGCTGAGACAGATAG 464

QY 455 cgsaagtgtagagtgatgtcatgtgcaatggtgttatgcatagagatttgaagcctgaga 514
Db 465 CTAAGGGGCTAGAGGGGCTACAGGGGCAAGTATAGTTCACAGGAGCTTGAAACCCAGAGA 524

QY 515 attctgtttgtcaacaagaagaaattctgcacttaagctattgatttgggtttat 574
Db 525 ACTGCTATTTCTTGACACAGAGTGAAGATCACCGTTGAAGATTATGGATTTGGGGCTGA 584

QY 575 ctgttctctttaacctggagagaggtttacagagattgttggaagtcctattatatg 634
Db 585 GTTCTATTGAGGATTTTGCAATCCAGTGGTGGTTTGGTTGGTTCATAGATTATGCTAT 644

QY 635 ctccagaag--tgtgaagagaattatggaacagaggttgatgtgtgagtgctggag 691
Db 645 CACCAGAAGCAGCTTTCAAGGGAAATATATACACCACTAAAGATGATATTTGGTCACTTGGTG 704

QY 692 ttatctctctactctgt 751
Db 705 TTATCTTTACATCTCCTCTCTGGGGTACCCACCTTTTCATCGCGCGCTCAATCGAAAA 764

QY 765 tggctcttgcattcttggaggggagttcttgattttaagagagatccttggctgcagatat 811
Db 775 AGCAACAATATGATTAATTAATGGGAGTTCAGTTTGTGAGAAAAACCTGGAAAAACATAT 824

QY 812 cagagagcgaagagagccttgtgaagcagatgttggaaacctgattcaactaagcgttga 871
Db 825 CTTATCGGGCAAAACCACTAATTTCCAGTCTCTTGAAGATTGATCCCTAACATGAGGGCTA 884

QY 872 ctgctcagaagttcttctgtatcacccttggat 902

FILE DATE: 10/11/94
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,449
FILING DATE: October 14, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Alan. E.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-45000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1776 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: Tobacco CCaMk cDNA and deduced amino-acid
FEATURE:
NAME/KEY: protein-coding sequence (not including
NAME/KEY: Stop codon)
LOCATION: nucleotides 20-1570
US-08-655-352-10

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2002, 23:35:04 ; Search time 1526.19 Seconds
(without alignments)
7181.736 Million cell updates/sec

Title: US-08-989-881-1

Perfect score: 1020

Sequence: 1 gttgtaaacacgncagt.....gcttgccgtatcatgtcat 1020

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estfun:*

2: em_esthum:*

3: em_estlin:*

4: em_estom:*

5: em_estpl:*

6: em_estba:*

7: em_estro:*

8: em_estov:*

9: em_htc:*

10: gb_estl:*

11: gb_est2:*

12: gb_htc:*

13: gb_gss:*

14: em_gss_fun:*

15: em_gss_hum:*

16: em_gss_inv:*

17: em_gss_pin:*

18: em_gss_pro:*

19: em_gss_rod:*

20: em_gss_vrt:*

21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	424.6	41.6	471	CNS00MGW	AL080606 Arabidops
2	407	39.9	833	BE641223	BE641223 Cri2.2.K0
3	378	37.1	659	AW685409	AW685409 NF029A07N
4	352.4	34.5	594	AI896274	AI896274 EST265717
5	343.2	33.6	656	BE523895	BE523895 M43C3STM
6	339	33.2	350	BE523895	BE523895 NF077A07E
7	336.4	33.0	590	AW443165	AW443165 EST308095
8	333.2	32.7	515	BE435148	BE435148 EST406226
9	333	32.6	455	CNS00ROC	AL087354 Arabidops
10	331.6	32.5	641	AW223685	AW223685 EST300496
11	315	30.9	666	AI054550	AI054550 coau0001F
12	301.6	29.6	657	BE584245	BE584245 6-12E-HA

c	13	299.4	29.4	644	10	BE443407
	14	294	28.8	685	11	BE454189
	15	291.4	28.6	601	10	AW043082
	16	284.6	27.9	731	10	AW256503
	17	282	27.6	501	10	AW931540
	18	279.4	27.4	732	10	AW387032
	19	278.6	27.3	742	11	BE596613
	20	275	27.0	748	11	BE123404
	21	270.6	26.5	582	11	BE616793
	22	267.4	26.2	689	10	AW217987
	23	264.2	25.9	664	10	AW684367
	24	263.4	25.8	608	11	BE140058
	25	263.2	25.8	659	10	AW686132
	26	260.8	25.6	635	10	AW587489
	27	259.8	25.5	742	11	BE1305348
	28	257.6	25.3	758	11	BE365168
	29	257.4	25.2	559	10	BE443788
c	30	257	25.2	687	11	BE600015
	31	255.2	25.0	583	10	AW671890
	32	254.2	24.9	662	10	AW685986
	33	253.6	24.9	718	11	BE126469
	34	253.4	24.8	561	11	BF097701
	35	253	24.8	680	11	BF644542
	36	248.2	24.3	542	10	AW441707
	37	246	24.1	663	11	BF646490
	38	246	24.1	664	11	BF648169
	39	244.6	24.0	759	11	BE365167
	40	242.6	23.8	592	10	AW035209
	41	242.2	23.7	585	11	BE140443
	42	241.8	23.7	681	11	BE368645
	43	237.4	23.3	652	11	BF646537
	44	235.4	23.1	461	11	BF588161
	45	233.4	22.9	456	11	BF651257

ALIGNMENTS

RESULT 1

CNS00MGW	471 bp	DNA	GSS	28-JUN-1999
LOCUS	Arabidopsis thaliana genome survey sequence Sp6 end of BAC F1H12 of			
DEFINITION	IGF library from strain Columbia of Arabidopsis thaliana, genomic			
	survey sequence.			
ACCESSION	AL080606			
VERSION	AL080606.1	GI:5281746		
KEYWORDS	GSS.			
SOURCE	thale cress.			
ORGANISM	Arabidopsis thaliana			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
	Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.			
REFERENCE	1 (bases 1 to 471)			
AUTHORS	Salanoubat M., Choisme N., Artiguenave F., Brottier P., Wincker P.,			
	Samson D., Saurin W., Weissenbach J. and Quetier F.			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 471)			
AUTHORS	Genoscope.			
TITLE	Direct Submission			
JOURNAL	Submitted (25-JUN-1999) Genoscope - Centre National de Sequenage :			
	BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr			
FEATURES	Location/Qualifiers			
Source	1. .471			
	/organism="Arabidopsis thaliana"			
	/strain="Columbia"			
	/gb_xref="taxon:3702"			
	/clone_lib="IGF"			
	/clone="F1H12"			
	/note="end : Sp6"			
BASE COUNT	132 a 83 c 120 g 136 t			
ORIGIN				

Query Match 41.6%; Score 424.6; DB 13; Length 471;
Best Local Similarity 99.1%; Pred. No. 6e-111;
Matches 427; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 163 ggaatcagctatctttgtacagatagagagactcgtgaagcttttagcttgcacatcaatc 222
Db 1 GGAATCAGCTATCTTTGTACAGATAGAGAGACTCGTGAAGCTTTAGCTTGCAATCAATC 60

QY 223 tccaagagaagctccgaacccgcgtcgtatgtgaagacgtccgtcgtgaagtcacagtc 282
Db 61 TCCRAGAGAGCTCCGACCCGCGCTCGATGTGGAACACGTCGCTCGTGAAGTCACCATC 120

QY 283 atgtcaactttacgggaacaccccaaacgctttgtgaacttaaaagcacttatgagataac 342
Db 121 ATGTCAACTTTACCGGAACACCCCAACGCTTGTGAACCTTAAAGGACTTATGAGAGTAAC 180

QY 343 gaggacctgcatcttggaggagctttgtgaagagagtgagctttttgtcggattgtt 402
Db 181 GAGAACGTGATCTGTGATGAGAGCTTTGTCAAGGAGGTGAGCTTTTGTGATCGGATGTT 240

QY 403 gcaagaggacattatcacagagcgtgcggcgctaccgtcgcgagacgacgacgagagtt 462
Db 241 GCCAGAGGACATATACAGAGCGTGCAGCGCTACCGTCGCGAGAACGATCGCGGAGGTT 300

QY 463 gtgaggatgtcatgtcaatgtgtttatgcataagagatttgaagcctgagaaattcttg 522
Db 301 GTGAGGATGTCTATGTCAATGTGTGTATGCATAGAGATTGAAGCCTGAGATTTCTTG 360

QY 523 ttgtctaacgaagagagaaattctgcaacttaagctattgattttgtttatctgtctc 582
Db 361 TTGTCTAACGAAGAGGAGAAATCTGCACCTTAAGGCTATTGATTGTTTGTATCTGTCTC 420

QY 583 ttttaaacctgg 593
Db 421 TTTTAAACCTGG 431

RESULT 2

LOCUS BE641223 833 bp mRNA EST 01-SEP-2000
DEFINITION Cr12_2_K07.SP6 Ceratopteris Spore Library Ceratopteris richardii
CDNA clone Cr12_2_K07_5, mRNA sequence.

ACCESSION BE641223
VERSION BE641223.1 GI:9958885
KEYWORDS EST.
SOURCE Ceratopteris richardii.
ORGANISM Ceratopteris richardii.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Filicophyta; Filicopsida; Filicales; Pteridaceae; Ceratopteris.

REFERENCE 1. (bases 1 to 833)
Chatterjee,A., San Miguel,P., Stout,S.C., Banks,J. and Roux,S.J.
Expressed sequence tags of cDNA clones from a C. richardii library
Unpublished (2000)
Contact: Roux SJ
Section of Molecular Cell and Developmental Biology
University of Texas
Biology Building, Room 16, Austin, TX 78712, USA
Tel: 512 471 4238
Fax: 512 232 3402
Email: sroux@uts.cc.utexas.edu
Plate: Cr12_2 row: K column: 07
Seq primer: SP6.

FEATURES

Source
1. .833
Location/Qualifiers
/organism="Ceratopteris richardii"
/cultivar="Brogn"
/db_xref="taxon:49495"
/clone="Cr12_2_K07"
/clone_lib="Ceratopteris Spore Library"
/tissue_type="Gametophyte"
/cell_type="Spore"
/dev_stage="20 hours after germination initiation"

RESULT 3

AW685409
LOCUS AW685409 659 bp mRNA EST 15-JUN-2000
DEFINITION NF029A07.NR1F1000 Modulated root Medicago truncatula cDNA clone
NF029A07.NR 5', mRNA sequence.
ACCESSION AW685409
VERSION AW685409.1 GI:7560145
KEYWORDS EST.

/note="Vector: pCMVSPORT6; EST sequence from cDNA library.
cDNA library constructed from mRNA isolated from C.
richardii spores that had developed for 20 hours after
their germination had been initiated by white light."

BASE COUNT 239 a 159 c 210 g 225 t
ORIGIN

Query Match 39.9%; Score 407; DB 10; Length 833;
Best Local Similarity 70.3%; Pred. No. 7.4e-106;
Matches 545; Conservative 0; Mismatches 230; Indels 0; Gaps 0;

QY 144 actcgttcgcgcgcgaattcgaatcacgctatctttgtacagatagagagactcgtgaagc 203
Db 11 ACTTGGTCTGGTGAATTTGGCATCACTTATTATGACAGATCGGAGACTGACGAAGT 70

QY 204 tttagcttgcacaaatcaatctccaagagaaagctccgaaccgcgcgtcgtatgtgaagacgt 263
Db 71 GCTAGCATGTAAATCTATTTCTAAAGGGAAGCTTTAGGACACCCATAGACATTGGAATGT 130

QY 264 cgcgtcgtgaagtcacgacatcatgtcaactttaccgggaacacccaaacgtttgtgaactaa 323
Db 131 TCGAAGAGAGGTGGATATTATGAGACATCTTCTTAAACATCCAAACATTGTGACTTTGGA 190

QY 324 agcgaacttatgagataaacgagaccgtgcactttgtatgagagctttgtgaagaggtga 383
Db 191 AGGGTCTATGAGATGAGAAATGCGTGCATCTTGTTCATGGAACATATGTGAAGGTGGTGA 250

QY 384 gcttttggctgcgattgttccaagagagacattatcacagagcgtgcgcgcgtaccgtcgc 443
Db 251 ATTGTTCGATCGCATTTAGCAAGAGGTCACTACAGGAGAGAGCTGCACGTCGGTTCAT 310

QY 444 gagaacgacgcgcgaagctgtgaggatgtgcacatgtgcacatgttgcacatgtgcacatgt 503
Db 311 GCCTACCATCTTGAAGTTTGCAGGTTTGCATAGGATAGGATAGGATAGGATAGGATAGG 370

QY 504 gaagcctgagaattcttcttgaacgaagagaaattctgcacttaagctattga 563
Db 371 TAGCCAGAAATTTCTGTTTGCACAAAGAAAGAAATTCGCCCTTAAGGCTATTGA 430

QY 564 ttttggcttatctgttctttaaaccctggagagaggtttacagagagattgttgaagctc 623
Db 431 TTTTGGATTATCCATCTTCTTCAACCTGGGAGAGTTCACGAATAGTAGGAAGTCC 490

QY 624 ttattatatgctccgaagagtggtgaagagaaattatggaccagagaggttgcgtgagag 683
Db 491 ATACTATATGGCACCTGAGTACTGAAAAGAGCTTATGGCCAGAGTTGATATATGAG 550

QY 684 tgcgtgagttatctctacatctgtcttcttgcctccgttttggcagagactga 743
Db 551 TGCAGGAGTTATATTACATTTCTTTATGCGGAGTCCCTTTTGGCTGAGACCGA 610

QY 744 acaagtggtgcttgcctatcttggagggaggttcttgcattttaagagagatccttggct 803
Db 611 ACAATTAGTAGCCAGCCCATCTTACGTGGAATGTGGAACTTACACAGAGATCCTTTGGCC 670

QY 804 gcagatatcagacgacgacaaagacgttgcgaagagatgttgaacacctgattcaactaa 863
Db 671 AATGTTTTCAGAAAATGCTTAAGCGTAGTGGCGCAAAATTTGGACCAAGATCCAAAGCA 730

QY 864 ggcgttgactgctcagcaagttcttgcacacctgttgatcacagatgcacagaaagaa 918
Db 731 AAGATTGACAGCTCAACAAGTCCCTTGCATTCATTCGCTGCTGTGAAATGCAAGAAA 785

Db 121 CAGCTCGGTGACTCCCAAAATGTTGAAGTGAATTCAGATGTCCTAATAGCAGTGGAGTTA 180
QY 491 tgcataagagattgaagcctgagaattcttctgttctaacagaagagagaattctgcac 550
Db 181 TGCATCGGACCTCAAGCCTGAAATTTCTGTGTTGAAACAAAGAAAGACAGACACCAT 240
QY 551 ttaagcctattgatttggtttatctctctctctctctctctctctctctctctctctctct 610
Db 241 TGAAGCAATGATTTGGTCTCTCAGTATTTCTTAAAGCCTGGTGAAGATTTAAACGAA 300
QY 611 ttattgaaagctcttattatgctctccagaaagctgttgaagaaattatgagaccagag 670
Db 301 TTGTGGAAAGTCGTACTCAATGGCCCGAGGTGCTGAGAGAGACTATGTTCCAGAG 360
QY 671 ttcattgtggaagcgtgagtgattctctctctctctctctctctctctctctctctctctct 730
Db 361 TAGATGCTGGAGTGTGGAGTAATTTCTTACATCTTGTATGTTGTTGTTCCACCATTT 420
QY 731 gggcagagactgaacagtggtgctctgcccattctgcccattctgagggagttctgtttaaga 790
Db 421 GGCACAAACTGAACAAAGATGTCACAGCAATCAATGCTGTTGTTGAAATTTAAAA 480
QY 791 gagatcttggtgcagatatacagagagcgaagccttgaagcagagattgtggaac 850
Db 481 GGGACCTTGGCCTAAGTATCCGACAATGCAAAAGACCTTGTGAAGAGATGCTTAACC 540
QY 851 ctgattcaactaagcgttgtagctgctcagcaagcttctgatacacccttgatcac 904
Db 541 CTGATCTAGCCCGAGGCTTACTGCTCAAAAAGTTCTAGATCATCCCTGGATAC 594

RESULT 5
BF647650 656 bp mRNA EST 20-DEC-2000
LOCUS NF077A07EC1F052 Elicited cell culture Medicago truncatula cDNA
DEFINITION BF647650
ACCESSION BF647650
VERSION BF647650.1 GI:11912780
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 656)
Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation -
Center for Medicago Genomics Research
Unpublished (2000)
Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert Length: 656 Std Error: 0.00
Plate: 077 row: A column: 07
Seq primer: TCACACAGGAACAGCTATCAC.
Location/Qualifiers
1. .656
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone_lib="NF077A07EC"
/tissue_type="Elicited cell culture"
/dev_stage="Cell suspensions derived from root tissues"
/note="Cells were induced six days after subculture"
/note="Vector: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to 50ug/ml glucose in the

final concentration. Samples were taken at 0.5, 1, 12 and 24 hours after induction. Equal amounts of RNA from each time point were pooled and used for mRNA isolation.

BASE COUNT 206 a 96 c 162 g 188 t 4 others
ORIGIN

Query Match 33.6%; Score 343.2; DB 11; Length 656;
Best Local Similarity 72.5%; Pred. No. 1.4e-87;
Matches 469; Conservative 0; Mismatches 176; Indels 2; Gaps 2;

QY 113 agatcagcacaagctcatcttagcagcagaactcgtgcgcgaattcgggaatcac-g 171
Db 8 AGATATTACAACAATAGCAATAGGAGAGAAATAGGAGAGAGAAATTTGGATACACNG 67
QY 172 tatctgttacagatagagagact-cgtgaagcttttagcttgcacaaatcattcocaagag 230
Db 68 TATTTATGTAAGATAGAGAAACNGGAGAGAAATAGCTTGTAAATCGATTTCAAAGGA 127
QY 231 aaagctccgaacccgcgtgagtggaagacgtccgtggaagtcacatcatgtcaac 290
Db 128 TAAGCTAAAGAACAGCGATTGATTTGAAGATGTTAGAAGAGAGGTTTGAATTAAGAGCA 187
QY 291 ttaccggaacaccccaaacgcttgtaaaccttaagcgacttatgagagataaacgagaccgt 350
Db 188 TTACCTTAACATCCTTAATATTGTTAGCTTGAAGGATACATTAAGAAGATGATGATAATGT 247
QY 351 gcatcttgtagagagcctttgtaagagagtgagccttttgcgcgattgtgcaagagag 410
Db 248 TCACTTGTGTATGGAGCTTTGTGAAGTGGTGAGCTTTTGTATCGGATTTGTCTAAGGG 307
QY 411 acattacagagcgtgcgcgcgtaccgtccgcgagaacgactcgcggaagttgtgagat 470
Db 308 ACAATTATACCGACGCGCCCGCGGCTGGTTAGACCATCGTTCAAGTTCTCAGAT 367
QY 471 gtgtcatgtcaatggtgttatgcatagagatttgaagcctgagaattcttctgttgotaa 530
Db 368 GTGCCACGAAACATGTTGTGATGCATCGGGATCTCAACCCGAGAACTTTTGTGTCAAA 427
QY 531 caagaaggagaattctgcacttaagcctattgatttgccttgccttgccttgccttgcct 590
Db 428 CAAGAAGGAACATCACTTTGAAAGCTATTGACTTTGTTGCTAAATACCTTTAAACC 487
QY 591 tggagagaggtttacagagagatttgaagccttattatgagcctcagagagttgtgaa 650
Db 488 AGTGATATAATTTAACGAGATAGTTGGAGTCCATATACATGCCCCCTGAAGTATGAA 547
QY 651 gagaaattatgaccagagaggttgatgtgtgagtgctgaggttatcctctacattctgt 710
Db 548 GAGAAATATGCGCTGAAATAGATATCTGAGTGGCGGAGTAATTTCTTTACATCTTACT 607
QY 711 ttgtgtgttcctccgttttggcagagactgaacaggtgtgtgctc 757
Db 608 TTGTGNATCCCTCCCTTTTGGGCANAACTGAGCAGGGGAATGCTC 654

RESULT 6
BE523895 350 bp mRNA EST 19-MAR-2001
LOCUS M43C3STM Arabidopsis developing seed Arabidopsis thaliana cDNA
DEFINITION BE523895
ACCESSION BE523895
VERSION BE523895.1 GI:9781873
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 350)
White, J.A., Todd, J., Newman, J., Focks, N., Girke, T., Martinez de
Ibarra, O., Jaworski, J.G., Ohlrogge, J. and Bening, C.
A new set of Arabidopsis expressed sequence tags from developing

seeds. The metabolic pathway from carbohydrates to seed oil
Plant Physiol. 124 (4), 1582-1594 (2000)

JOURNAL MEDLINE COMMENT

Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
Michigan State University
224 Biochemistry, Michigan State University, East Lansing, MI 48824
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Tel: 517 355 1609
Fax: 517 353 9334
Email: benning@msu.edu
Michigan State University DNA Sequencing Facility Arabidopsis
Biological Resource Center, The Ohio State University, 309 Botany &
Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX:
6142922603 TEL: 6142923371.

FEATURES

source

Location/Qualifiers

1..350

/organism="Arabidopsis thaliana"

/strain="Columbia"

/db_xref="taxon:3702"

/clone="M43C3"

/clone_lib="Arabidopsis developing seed"

/tissue_type="seed"

/dev_stage="5-13 days after flowering"

/lab_host="E.coli"

/note="Organ: Developing seed; Vector: pBluescript SK-;

Site_1: EcoRI; Site_2: XhoI"

95 a 69 c 101 g 85 t

BASE COUNT

ORIGIN

Query Match 33.2%; Score 339; DB 10; Length 350;

Best Local Similarity 98.6%; Pred. No. 2e-86; Indels 0; Gaps 0;

Matches 342; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 151 cgcggcaattcggatcgcgtatctttgtacagatagagagactcgtgaagcttttagct 210

Db 4 CGAGGCGAATTCGGAATCAGTATCTTTGTACAGATAGAGAGACTCGTGAAGCTTTAGCT 63

QY 211 tcaaatcaatctccaaagaaagctccgaacccgcgtgatgtgaaagcgtccgtcgt 270

Db 64 TCGAAATCAATCTCCAAAGAAAGCTCCGAAACCGCGTCGATGTGGAAGACGTCGCGTCT 123

QY 271 gaactcacatcatgtcaactttaccgaacacccaaacgttgtgaaacttaagagact 330

Db 124 GAGTCCAGATCATGTCTACTTTTACCGAACACCCCAACCTTTGTGAACCTTTAAGCGACT 183

QY 331 tatgagataacagagacgctgcatcttctgtatgagcgtttgtgaaaggaggtgagctttt 390

Db 184 TATGAGGATAACGAGAACGTCATCTTGTGATGAGCTTTGTGAAGAGGTGAGCTTTT 243

QY 391 ggtcgattgttgcagagagacattatagagagcgtgcggcgctaccgtcgagagacg 450

Db 244 GATCGGATTTGTCAGAGAGACATTTACAGACGCTGCGCGCTACCGTCGCGAGAACG 303

QY 451 atcgcggaagtgtgaggtgtgtcatgtcaatgggtgtatgcatag 497

Db 304 ATCGCGGAGGTTGTGAGGATGTCTCATGTCAATGGGTATGATGATAG 350

RESULT

AW443165

LOCUS

DEFINITION

EST308095 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA

clone cLET43E12 5', mRNA sequence.

AW443165

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

REFERENCE AUTHORS

1 (bases 1 to 590)

D'Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E.,

Liang,F., Hansen,T.S., Ronning,C.M., Craven,M.B., Bowman,C.L.,

Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D., Giovannoni

,J.J. and Martin,G.B.

Generation of ESTs from tomato callus (mixed elicitor)

Unpublished (1999)

Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>

5 prime sequence.

Location/Qualifiers

1..590

/organism="Lycopersicon esculentum"

/cultivar="Rio Grande PtoR"

/db_xref="taxon:4081"

/clone="cLET43E12"

/clone_lib="tomato mixed elicitor, BTI"

/tissue_type="leaf"

/dev_stage="4-6 week old plants"

/lab_host="Xl1-Blue MRF"

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:

XhoI; cLET - Inoculated with a variety of disease response

elicitors. Plants exposed to 2.6 dichloroisocytin

acid, BTH, jasmonic acid, ethylene, fenthion, EIX, EcoRI

okadaic acid, or systemin prior to tissue harvest.

site was destroyed during cloning."

164 a 100 c 153 g 173 t

BASE COUNT

ORIGIN

Query Match 33.0%; Score 336.4; DB 10; Length 590;

Best Local Similarity 73.4%; Pred. No. 1.2e-85;

Matches 430; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

QY 329 cttatagagataacgagacgctgcacatctctgtgatgagctttgtgaaggaggtgagcttt 388

Db 5 CGTGTGAGGATGAAATTCGCGTTCATTGTGTGATGGAACCTATGTGAAGGTGGTGAAGTGT 64

QY 389 ttggtcggatgtgtcaagaggacattatcacagcgtgcggtgcgtaccgtgcgcgagaa 448

Db 65 TTGATGAGATCGTGTCTAGGGGCGCATTTACTGACAGCAGCAGCTGCTGTACACGGA 124

QY 449 cgatcgcgggaagttgtgaggtgtgcattgcattggtttatgcatagagatttgagac 508

Db 125 CGATTGTGGAGGTGTGCAGCTTTGTCAAAACATGGAGTGATTTCATAGAGATTGGAAGC 184

QY 509 ctgagaattttctgttgttaacaagaaggagaattctgcacttaagctattgattttg 568

Db 185 CCAGAACTTTTGTGTGTAATAAGAAAGGAAATTCACCTCTTAAGCAATGATTGTTG 244

QY 569 gttattctgttctcttaaacctggagagaggtttacagagattgttgggaagctctatt 628

Db 245 GCITGTCAATCTTCTCAAGCCAGGTGAGAGTTCTCCGAATAGTTGGAAGTCCATATT 304

QY 629 atatggtccagaagtgttgaagagaaattatgacagagaggttgatgtgtgagtgctg 688

Db 305 ATATGGCTCTGAGGTGCTCAAAACGAAACTATGACAGAAATAGATATATGAGAGTCAG 364

QY 689 gattatcctctacatctctgtgtgtgttctcctcgttttgggagagagactgaacaag 748

Db 365 GAGTCATTTATATATTTTGTATGTTGGGGTTCCTCCTCTTTGGGCTGATCTGGAACAG 424

QY 749 gttgtggtcttgcacatcttgaggggagttcttatttaagagagatccttgcgcaga 808

Db 425 GTGTGCCCAAGCCATTTTACGTGGGGCAATTGATTTCAAACGGAACCCCTGGGCTAGTA 484

QY 809 taccagagagcgaagagcctgttgagcagatgttggaaacctgattcaactaagcgtt 868

Db 485 TTTCAGAAAGGTGCTTAAATAATCTTGTGCAGGCAAAATGTTAGAGGCGACATCCAAAGCTTCGAC 544

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QY 869 tgaactgcagcaagtcttgcatacccttgatcacagaaatgcaaa 914
Db 545 TGTCTGCAAGCAAGTGTGAGTGAACACCCCTGGCTTCAAAATGCTAA 590

RESULT 8
LOCUS BE435148 515 bp mRNA EST 18-MAY-2001
DEFINITION EST406226 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
clone cLEG25A6, mRNA sequence.
ACCESSION BE435148
VERSION BE435148.1 GI:9432991
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 515)
AUTHORS Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,I.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
,S.D.
TITLE Generation of ESTs from tomato fruit tissue, breaker stage
JOURNAL Unpublished (2000)
COMMENT Contact: CUGI
Clemson University
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES
Source
1..515
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEG25A6"
/clone_lib="tomato breaker fruit, TIGR"
/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
note="Vector: pBluescriptSKMCladapt; Site_1: EcoRI;
Site_2: XhoI; Fruit were harvested at the breaker stage
(first sign of lycopene accumulation on the blossom end of
the fruit). Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
BASE COUNT 139 a 74 c 142 g 160 t
ORIGIN
Query Match 32.7%; Score 333.2; DB 10; Length 515;
Best Local Similarity 78.0%; Pred. No. 1e-84;
Matches 401; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

QY 304 ccaaacgttgcgaacttaaacgcgacttatgagataaacgagaccgtgcattgtgatg 363
Db 2 CCAAAATATCTGGAAGTGTGAGCTACTTATGGAAGTAATGAAGCAGCTCATCTGTATG 61

QY 364 gactttgtgaaggagtgagctttttgtgcgagattgttgcagagaggaacattatacagag 423
Db 62 GAGTATGTGAAGTGGGGAGTGTGATGATAGAATTGTAGTAGAGGGCATACAGTGAA 121

QY 424 cgtgcggcgactaccctgcgagaaagatcgcggaagttgtgaggtgtgtcatgtcaat 493
Db 122 AGAGCTCAGCTGGGTGCGCAAACTGTATGACAGAAATTGTAAGGATGTGTCATGCTAAT 181

QY 484 ggtgttatgcatagagatttgaagcctgagaatttctgtttgtctaaagaagagaat 543
Db 182 GGGGTATGATAGAGACTTGAACCTGACAAATTTTCGTTGCTTAATAAGAAAGACAT 241

QY 544 tctgcacttaagactattgatttggtttatctgttctctttaaactggagagaggtt 603

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Db 242 TCTGCTCTTAAGCCATCGATTTTGCCCTATCTGCTTTTCAAGCCTGGTGAAGATTTC 301
QY 604 acagagattgttggaagtccttattatatgtctccagaagtggttggaagagaattatgga 663
Db 302 TCTGAGATTGTGGGAAGTCCATACTACATGGCACCAGAGGTGTGAAGCGGAATTATGGA 361
QY 664 ccagaggttgatgtgtggaagtgcaggtatctctacatctcttgcattgtgtgttct 723
Db 362 CCAGAAGTTGATTTGGAGTGTGCTGTGTCATCTTATATTGTTATGTGGGGTTCCT 421
QY 724 ccgttttgggcagagactgaacaaggtgtggtcttgcctcttgcaggttggtgtat 783
Db 422 CCATTTTGGCTCAAACTGACAAAGAGTGTCTCTTTCAATTTTAAGGGAGTGATAGAT 481
QY 784 tttaagagagactccttggtgcagatatcagaga 817
Db 482 TTCAAGAGGGAACCATGGCTCAAGTCTCTGAAA 515

RESULT 9
CNS00ROC 455 bp DNA GSS 28-JUN-1999
LOCUS Arabidopsis thaliana genome survey sequence SP6 end of BAC F14D16
DEFINITION of IGF library from strain Columbia of Arabidopsis thaliana,
genomic survey sequence.
ACCESSION AL087354
VERSION AL087354.1 GI:5288494
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 455)
AUTHORS Salanoubat,M., Choisme,N., Artiguenave,F., Brottier,P., Wincker,P.,
Samson,D., Saurin,W., Weissenbach,J. and Quetier,F.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 455)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segreg@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
FEATURES
Source
1..455
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone_lib="IGF"
/clone="F14D16"
/note="end : SP6"
BASE COUNT 129 a 117 c 81 g 128 t
ORIGIN
Query Match 32.6%; Score 333; DB 13; Length 455;
Best Local Similarity 84.3%; Pred. No. 1.1e-84;
Matches 375; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 95 ccatggctaatcaaacactcagatcagcgacaagtacatctcttagaagaaactcgtcgag 154
Db 445 CTATGAGCAATCAAACTCAGATCAGGCACAAATACATCTTAGTCTGTAATTAGTCGAG 386

QY 155 gcaaatccgaatacgaactatctttgtacagatagagagactcgtgaagcttagcttga 214
Db 385 GCGAATTGCGAATCACTTACCTCTGATCTGTAATGTAATGTAATGTAATGTAATGTAAT 326
QY 215 aatcaatctccaagagaaaagctccgaacccgtcgatgtggaagacgtccgtcgagag 274
Db 325 AATCGATTTCAAAGCGGAAGCTTCGAACACAGCTGTCGATATCGAAGACGCTTCGTCG 266
QY 275 tcacgatcatgtcaactttaccggaacaccccaacgctgtgaaacttaagacgacttatg 334

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Db 265 TAGCGATTATGCTACCTTACTGAGCATCCAAAGTAGTAAAGCTAAGCTAGTAG 206
Qy 335 aggataacgagaccgtgcatcttgatggagcttttggaaggaggtagctttttgtgc 394
Db 205 AGGATAACGAGAACGTGCATCTGTTATGAGAGCTTGTGGAAGGAGGTGAGCTTTTGATC 146
Qy 395 ggattgtgcaaggagacattatcacagagctgcggcggtaccgctcgcggaacgacgcg 454
Db 145 GGATTGTGTGTAAGAGCAATTACACGGAGCGTGTCTGTCGAGCTGTTCCGGAAGACGATTG 86
Qy 455 cggaggtgtgagagatgtcatgtcaatgtgttatcatagagatttgagcctcaga 514
Db 85 CTGAGTTGTGTAAGAGCAATTACACGGAGCGTGTCTGTCGAGCTGTTCCGGAAGACGATTG 26
Qy 515 attctgtttgtctaacaagaagga 539
Db 25 ATTCTCTGTTGCTAATAAAAAAGGA 1

RESULT 10
AW223685 641 bp mRNA EST 18-MAY-2001
LOCUS EST300496 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA
DEFINITION clone cLEN12D10, mRNA sequence.
ACCESSION AW223685
VERSION AW223685.1 GI:5535369
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 641)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,
Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Renning,C.M.,
Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato fruit tissue
Unpublished (1999)
Contact: CUGI
Clemson University
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES
Location/Qualifiers
1..641
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEN12D10"
/tissue_type="pericarp"
/dev_stages="red ripe (7-20 days post-breaker)"
/notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Giovannoni; Fruit were tagged at the
breaker stage (first sign of lycopene accumulation on the
blossom end of the fruit) and harvested 7 days
post-breaker (fully red-ripe), 10 days post breaker, and
20 days post-breaker (over-ripe). 20 day fruit which
showed external or internal signs of pathogenesis were
discarded. Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
BASE COUNT 181 a 111 c 162 g 187 t
ORIGIN
Query Match 32.5%; Score 331.6; DB 10; Length 641;
Best Local Similarity 73.9%; Pred. No. 3e-84;
Matches 421; Conservative 0; Mismatches 149; Indels 0; Gaps 0;
Qy 348 cgtgcacatcttgatggagcttttgaaaggaggtagcttttttgctcgatgttgcaag 407

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Db 7 CGGTCAATTTGGTGAATGAACATATGTAAGAGTGGTGAGCTGTTGTATAGATCGTTGCTAG 66
Qy 408 aggacattatacagagcgtcgggcggtaccgctcgcgagaacgatcgcggaagtgtgtgag 467
Db 67 GGGGCATTATACTGAACGAGCAGCTGCTGCTGTACACGGACGATTTGTGGAGGTTGTGCA 126
Qy 468 gatgtgcatgtcaatgggttatgcatagagatttgagcctgagaaattttcttttgc 527
Db 127 GCTTTGTCCAAACAATGGAGTGAATTCATAGAGATTGAAGCCCGAGAACTTTTGTGTC 186
Qy 528 taacaagaagagaaattctgcacttaagctattgatttggtttatctgttctcttaa 587
Db 187 TAATTAAGAAAGAAATTCACCTCTTAAGCAATTTGATTTGGCTTGTCAATCTCTTCAA 246
Qy 588 acctggagagaggtttcacagagattgttggagctcttatttatgtggtccagaagtgtt 647
Db 247 GCCAGGTGAGAAGTTCTCCGAAATAGTTGGAAGTCCATATATATGCTCTCGAGTGTCT 306
Qy 648 gaagagaaattatggaaccagaggttgatgtggagtgctggagttatccctacattt 707
Db 307 CAACGAAACTATGGACCAAGAAATAGATATATGAGTGCAGGAGTCATTTTATATATTTT 366
Qy 708 gctttgtggttctcctcgcttttggcgagagactgaacaagtggtgctcttgcacattt 767
Db 367 GTTATGTGGGTTCTCTCCCTTTTGGGCTGAATCTGAACAAGGTGTGCCCAAGCCATTTT 426
Qy 768 gagggagttcttattttaaagagagatccttggctgcagatatcagagagcgcaagag 827
Db 427 ACGTGGGCAATTGATTTCAAAACGGGAAACCCCTGGCTAGTATTTCAAGAGGTGTAAAAA 486
Qy 828 ccttgaagcagatgttggaaacctgattcaactaagcgtttgactgtcagcaagtct 887
Db 487 TCTTGTCAAGGCAATGTTAGAGGCAGATCCAAAGCTTCGACTGTCTGCAAGCAAGTACT 546
Qy 888 tgatcaccttggtacacagaatgcaaaqaa 917
Db 547 TGAACACCTTGGCTTCAAAATGCTTAAGAA 576

RESULT 11
AI054550 666 bp mRNA EST 16-JUL-1998
LOCUS coau0001F17 Cotton Boll Abscission Zone cDNA Library Gossypium
DEFINITION hirsutum cDNA clone coau0001F17 5', mRNA sequence.
ACCESSION AI054550
VERSION AI054550.1 GI:3325664
KEYWORDS EST.
SOURCE upland cotton.
ORGANISM Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; euroids II; Malvales; Malvaceae; Gossypium.
1 (bases 1 to 666)
Wan,C.-H., Yu,Y., Sasinowski,M. and Wing,R.A.
Cotton EST Database: Sequence Analysis of 2000 cDNA Clones from an
Abscission Zone Library
Unpublished (1998)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: SP030 (AACAGCTATGACCATGATTA)
High quality sequence stop: 282.
FEATURES
Location/Qualifiers
1..666
/organism="Gossypium hirsutum"
/db_xref="taxon:3635"
/clone="coau0001F17"
/clone_lib="Cotton Boll Abscission Zone cDNA Library"
Source

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/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF097G08LF"
/clone_lib="Developing leaf"
/tissue_type="leaf"
/dev_stage="Pooled developmental"
/notes="Vector: Lambda Zap; Contains a mixture of very
young, developing, mature and senescing leaves."
BASE COUNT      203 a      92 c      164 g      224 t
ORIGIN

Query Match      28.8%; Score 294; DB 11; Length 685;
Best Local Similarity 66.4%; Pred. No. 1.9e-73;
Matches 437; Conservative 0; Mismatches 220; Indels 1; Gaps 1;

QY 291 ttaccggaacacccaacgctgtgaaacttaagcgacttatgagataacgagacgct 350
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 TTTGAGTGTCAACCAAAATATTGTTGAATTTAAAGGAGCTTATGAGATAGGAATTCAGT 60

QY 351 gcaatcttgatgagagctttggaaggagtgagc-tttttgctogagattgttgaagag 409
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db -61 TCATGTGTGTTGAAGACTTGTGCTGTGTGTAACNTTTTTGTATGAGATCATTTGCTAAAG 120

QY 410 gacattatacagagcgctgcgcgcgtaccgtgcgcgagaaacgatcgcggaagtgtgagaa 469
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 GACATTATAGTGAAGAGCTGTCTCTATTGTGACAGAGATGTTAATGTGTGTAATA 180

QY 470 tbtgtcatgcaatgdtgttatgcataagatttgaagcctgagaattcttctgtttgcta 529
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 TTGTGCTATTTATGGGAGTTATGCATAGGGATCTGAACACAGAGAATTTCTTTGTGCTA 240

QY 530 acaagaagagaaattctgcacttaagctattgatttgatttgatttctctcttaaac 589
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 GTAAGACATAAATGCACTCTTAAGGCTACTGATTTGTTGCTGTCTTTTCATTGAAG 300

QY 590 ctggagagaggtttacagagattgttggaagtcctattatatggctccagaaagtgtga 649
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 AAGGAAGGTGTATCGGATATAGTCGGAAGTCTTATTATTGTTGCTCAGAGTCTTTC 360

QY -650 agagaaattatgaccagaggttgatgtgtgagtgctgaggtatccctctacatttgc 709
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 GTCGTAGATCCGGAAAGAAATAGATATATGAGTGCAGAGTTATCTATATATCTTAC 420

QY 710 ttgtgagtgctccgttttggcagacactgaacaaagtgtggtcttggcattcttga 769
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db -421 TTAGTGTGTCTCCCTCCATTTTGGGCTGACACTGAAAGGGAATTTTGTATGCAATTTGG 480

QY 770 ggggagttcttatttaagagagatccctgtgcgagatacagagagcgcaaaagagcc 829
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 AAGGTCATATTGATTTTGAAGTGAACCGTGGCTTAAATTTTCAGACAGGCCCAAGATC 540

QY 830 ttgtgaagcagatgttggaacctgattcaactaagcgtttgactgctcgcgaagttcttg 889
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 TTGTCGTAATATGCTTATACAGGACCCGAAAGAACGCAATTCGCTGCACAGGTTCTAG 600

QY 890 atcacctttggatcacagaatgcaagaagaagatcaagcttatcatcacgtcgacct 947
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 601 AGCATCTTGGATTAAGATGTGTAATGCTTGTGATGAAGCAATAGACAGTGCAGTTCT 658

RESULT 15
AW043082
LOCUS
DEFINITION
ST29B03 Pine Triplex shoot tip library Pinus taeda cDNA clone
ACCESSION
AW043082
VERSION
AW043082.1
KEYWORDS
EST,
SOURCE
loblolly pine.
ORGANISM
Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.

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REFERENCE
AUTHORS      Whetten,R.W., Kinlaw,C.S., Retzel,E. and Sederoff,R.R.
TITLE        The Pine Gene Discovery Project
JOURNAL      Unpublished (1999)
COMMENT      Contact: Ross Whetten
              Forest Biotechnology Group
              North Carolina State University
              Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
              ,NC, 27695-8008
              Tel: 919-515-7800
              Fax: 919-515-7801
              Email: rosswhetten@unity.ncsu.edu
Seq primer: 5' lambda Triplex2 Sequencing Primer.
Location/Qualifiers
1. .601
/organism="Pinus taeda"
/db_xref="taxon:3352"
/clone="ST29B03"
/clone_lib="Pine Triplex shoot tip library"
/lab_host="E. coli BM25.8"
/notes="Organ: shoot tips; Vector: Lambda Triplex; Site_1:
SfiI (A); Site_2: SfiI (B); Shoot tips (approx. 2 cm from
apex) were collected during the spring, frozen and used
for mRNA isolation. The SMART-PCR method (Clontech) was
used to prepare a library from 1 ug total RNA, using the
lambda triplex vector. Plasmid subclones in pTriplex were
recovered by cre-lox excision in E. coli strain BM25.8 and
sequenced from the 5' end."
BASE COUNT      164 a      117 c      167 g      149 t
ORIGIN

Query Match      28.6%; Score 291.4; DB 10; Length 601;
Best Local Similarity 69.7%; Pred. No. 1e-72;
Matches 405; Conservative 0; Mismatches 175; Indels 1; Gaps 1;

QY 136 ggaacagaactcgtgcgcgcgaattcgaacacgtatctttgtacacataagaagact 195
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 17 GGAAGAGAGCTCGGAGGGGTGAGTTCGGCATTTACTCTTTGTACTGACAGGAGACT 76

QY 196 cgtgaagctttagcttgcaaatcaattccaaagagaagctccgaaccccgctcgatgtg 255
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 77 GAAGAAATGCTTGCCTGCAAGTCTATTTCGAAGCGGAAGCTCAGAACACGATAGATATC 136

QY 256 gaagacgtccgttggaagtcacgatcatgtcaactttaccggaaacacccaaactgttg 315
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 137 GAGGATGTGAGCGGAGAGTAGCTATAATGAACAATTTGCTCAGCATCCGAACATTGTT 196

QY 316 aaacttaagcgacttatgagataacgagacgtgcactctgtgtgagctttgtgaa 375
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 197 ACCTTGAAGCCACGTCACGAGGACGACAGCTGTGTCATCTCGTCATGAGAGCTCTCGAG 256

QY 376 ggaagtgaagcttttggctggattgttgaaggagacattatcacagagcgtgogcggt 435
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 257 GGTGGAGAGCTATTTCACAGGATCGTGTCTAGAGGCGCATTTACAGCGAGCGTGC CGGGCT 316

QY 436 accgtgcgagaaacgatcgcggaagtgtgagagatgtgcatgtcaatggtgttatgat 495
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 317 GCTGTGTACAGTACTATTGTTGAAGTGTTCAGATGTGTCAAAAACCGGGTGTGATGAT 376

QY 496 agagatttgaagcgtgagaattcttgttgcatacaagaagagaattctgcacttaag 555
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 377 CGGACCTCAACCTGAGAGATTTCTGTTGGGATATAAAAAGAGAGAAATTCACCTCTGAAG 436

QY 556 gctattgatttgggtttatctgtctcttaaaccttgagagaggtttacacagagattgtt 615
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 437 GCTATTGATTTCGGTCTTTCTGTGTTCTTTAAAGCCAGCGGCGGANTTTCTGAAATAATG 496

QY 616 ggaagtcctattatattggtccagaaggtgtgaagagaaattatggacacagagttgat 675
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 497 GGTAGCCCATATATACATGGCAAAAAGTCTCTGAAGCNGAACCTATGACCAAAAGGTGAT 556

QY 676 gtgtggagtgctggagttatctctacatctgtcttctgttg 716

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Db 557 -TTGGAGTGCAGGGTCATCCGTCANTTTATGNGTGGGG 596

Search Completed: March 3, 2002, 00:02:31
Job time: 1647 sec